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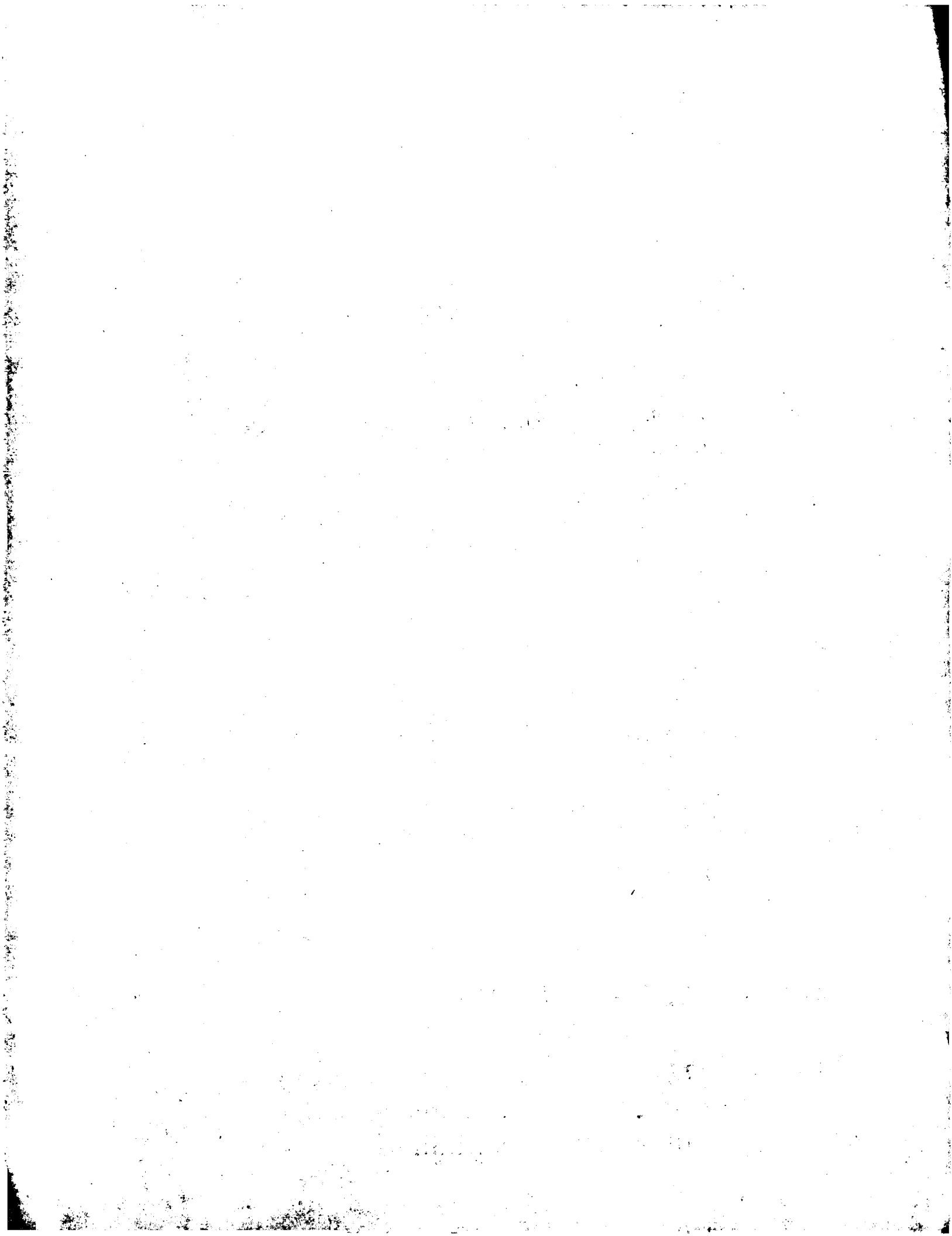
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! FINDPATTERNS on pir: allowing 0 mismatches
! 1 R(V,E) (N,D) LRI (A,L) L(R,E) YW(Q,D) S

May 5, 2003 1

Databases searched:
NBRF, Release 73.0, Released on 16Aug2002, Formatted on 20Aug2002

Total finds: 0
Total length: 96,134,422
Total sequences: 283,224
CPU time: 04:13.51

! FINDPATTERNS on swp:* allowing 0 mismatches
! 1 R(V,E) (N,D) LRI(A,L) L(R,E) YW(Q,D) S

May 5, 2003 1

Databases searched:

SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
SPTREMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002

Total finds: 0
Total length: 247,523,443
Total sequences: 784,472
CPU time: 11:48.22

! FINDPATTERNS on genpept: * allowing 0 mismatches
! 1 R(V,E) (N,D) LRI(A,L) L(R,E) YW(Q,D) S

May 5, 2003 1

Databases searched:
GENPEPT, Release 131.0, Released on 30Aug2002, Formatted on 31Aug2002

Total finds: 0
Total length: 348,344,575
Total sequences: 1,135,942
CPU time: 16:22.94

> O <
O| |O Intelligenetics
> O <

Quest - Quick User-directed Expression Search Tool.
Release 5.4

-- Outline of search "seq3-pat" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "new.key":

Selected sequence key from "new.key":
seq3 (AA) ID seq3 AA preliminary pattern

1 followed by
2 r
2 v or e
2 n or d
2 lrl
2 a or l
2 1
2 r or e
2 yyw
2 q or d
2 s

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries

-- Output Parameters --

Format Options:		File Options:	
Nucleic acid code matching	Exact	Indirect file	No
Find non-matching hits only	No	Sequence or key file	No
Report key used	Yes	List of hits	No
Note position of hit	Yes	Hit display	Yes
Display full annotations	Yes	Name and annotations	Yes
Sequence context	50		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:32.09	00:00:41.00
Number of sequences searched:		170751
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

> O <
O| |O Intelligenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq3-iss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence.

Selected sequence key from "new.key":
seq3 (AA) ID seq3 AA preliminary pattern

1 followed by
2 r
2 v or e
2 n or d
2 l r l
2 a or l
2 1
2 r or e
2 y y w
2 q or d
2 s

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:		File Options:	
Nucleic acid code matching	Exact	Indirect file	No
Find non-matching hits only	No	Sequence or key file	No
Report key used	Yes	List of hits	No
Note position of hit	Yes	Hit display	Yes
Display full annotations	Yes	Name and annotations	Yes
Sequence context	50		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:02:04.08	00:02:30.00
Number of sequences searched:		262643
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 13:59:50 ; Search time 15 Seconds
(without alignments)
89.725 Million cell updates/sec

Title: US-09-742-148A-3
Perfect score: 56
Sequence: 1 RXLRRLXLYYXWS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	66.1	354	2	180168
2	34	60.7	131	2	C91087
3	34	60.7	131	2	E85932
4	34	60.7	131	2	AG0863
5	34	60.7	131	2	141066
6	34	60.7	274	1	HLH032
7	34	60.7	274	1	A35997
8	34	60.7	743	2	T22251
9	33	58.9	253	2	T04435
10	33	58.9	273	2	I36509
11	33	58.9	274	2	I54463
12	33	58.9	354	2	I59308
13	33	58.9	354	2	I80167
14	33	58.9	355	2	I80169
15	33	58.9	355	2	I80171
16	33	58.9	357	2	I67482
17	33	58.9	359	1	HLH012
18	33	58.9	362	1	HLH088
19	33	58.9	362	2	B30345
20	33	58.9	362	2	JH0541
21	33	58.9	362	2	JH0539
22	33	58.9	362	2	JH0540
23	33	58.9	362	2	A45834
24	33	58.9	362	2	A45834
25	33	58.9	362	2	I62045
26	33	58.9	362	2	I84490
27	33	58.9	362	2	A30345
28	33	58.9	362	2	I59633
29	33	58.9	362	2	S24434

ALIGNMENTS

30	33	58.9	362	2	137120	MHC class I histoc
31	33	58.9	363	2	S07113	class I histocompa
32	33	58.9	363	2	S03537	class I histocompa
33	33	58.9	364	2	D35997	MHC class I histoc
34	33	58.9	365	2	S77963	MHC class I histoc
35	33	58.9	365	2	I54416	HLA-AW24 protein -
36	33	58.9	365	2	I54493	MHC class I histoc
37	33	58.9	760	2	A39233	hypothetical prote
38	32	57.1	218	2	G91207	probable replicase
39	32	57.1	223	2	A65172	hypothetical prote
40	32	57.1	310	2	H82138	probable phosphati
41	32	57.1	325	2	A86054	probable replicase
42	32	57.1	342	2	A36963	endoglucanase CMCA
43	32	57.1	365	2	I57814	MHC class I -alpha
44	32	57.1	416	2	D71923	hypothetical prote
45	32	57.1	416	2	C64590	hypothetical prote

RESULT 1
180168
Class I histocompatibility antigen - chimpanzee (fragment)
C/Species: Pan troglodytes (chimpanzee)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
C/Accession: 180168
R/McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wackin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A/Title: A uniquely high level of recombination at the HLA-B locus.
A/Reference number: 159308; MUID:94286544; PMID:8016085
A/Accession: 180168
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-354 <RES>
A/Cross-References: EMBL:U05579; NID:9454775; PIDN:AAA50182.1; PID:9454776
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F.212-277/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0.
Db 1 RXLRRLXLYYXWS 14
91 KENLRALRYTQS 104

RESULT 2
C91087
hypothetical protein EC83667 (imported) - Escherichia coli (strain O157:H7, substrain RI
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C/Accession: C91087
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
Gisawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-131 <HAY>
A/Cross-References: GB:BA000007; PIDN:BA837090.1; PID:Q13363139; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A/Genes: EC83667

Query Match
Best Local Similarity 50.0%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 5 RIXLXYXWS 14

DB 64 RISIMFYWSS 73

RESULT 3

E85932

hypothetical protein ygdD (imported) - Escherichia coli (strain O157:H7, substrain EDL93)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #ext_change 14-Sep-2001

C:Accession: E85932

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimianta, E.; Potamocostas, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85932

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-131 <STO>

A:Cross-references: GB:AE005174; NID:g12517286; PIDN:AG57921.1; GSPDB:GN00145; UNQIP:241

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ygdD

Query Match
Best Local Similarity 60.7%; Score 34; DB 2; Length 131;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 4

AG0863

conserved hypothetical protein STY3121 (imported) - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #ext_change 09-Nov-2001

C:Accession: AG0863

R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

Th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.W.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; PMID:11677608

A:Accession: AG0863

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-131 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD02807.1; PID:g16504061; GSPDB:GN00176

C:Genetics:

A:Gene: STY3121

Query Match
Best Local Similarity 60.7%; Score 34; DB 2; Length 131;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 5

I41066

hypothetical 14.3K protein (fucR-gcva intergenic region) - Escherichia coli (strain K-12

C:Species: Escherichia coli

C>Date: 31-May-1996 #sequence_revision 31-May-1996 #ext_change 01-Mar-2002

C:Accession: I41066; I41230; G65063; S34372

R:Everett, M.; Walsh, T.; Guay, G.; Bennett, P.

Microbiology 141, 419-430, 1995

A:Title: Gcva, a LysR-type transcriptional regulator protein, activates expression of th

eins.

A:Reference number: I41066; MUID:95219098; PMID:7704273

A:Accession: I41066

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-131 <RES>

A:Cross-references: EMBL:X73413; NID:g312765; PIDN:CA51814.1; PID:g312767

J. Wilson, R.L.; Stauffer, G.V.

J. Bacteriol. 176, 2862-2868, 1994

A:Title: DNA sequence and characterization of Gcva, a LysR family regulatory protein for

A:Reference number: I41229; MUID:94245611; PMID:8188587

A:Accession: I41230

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-137, '6' 35-131 <RE2>

A:Cross-references: EMBL:U01030; NID:g393004; PIDN:AC13743.1; PID:g523332

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G65063

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Accession: G65063

A:Molecule type: DNA

A:Residues: 1-131 <BLAT>

A:Cross-references: GB:AE00364; GB:U00096; NID:g2367162; PIDN:AC75849.1; PID:g1789172;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ygdD

Query Match
Best Local Similarity 60.7%; Score 34; DB 2; Length 131;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 6

HHU032

MHC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #ext_change 05-Sep-1997

C:Accession: A26088

R:Man, A.M.; Ennis, P.; Parham, P.; Holmes, N.

J. Immunol. 137, 3671-3674, 1986

A:Title: The primary structure of HLA-A32 suggests a region involved in formation of the

A:Reference number: A26088; MUID:87058961; PMID:2431040

A:Accession: A26088

A:Molecule type: protein

A:Residues: 1-274 <MAN>

C:Genetics:

A:Gene: GDB:HLA-A

A:Cross-references: GDB:119310; OMIM:142800

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

F136261/Domain: immunoglobulin homology <IMM>

F136261/Domain: immunoglobulin homology (Aa) (covalent) #status predicted

RESULT 7

A35997

MHC class I histocompatibility antigen HLA-A25 alpha chain precursor - human

C:Species: Homo sapiens (man)
 C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 16-Feb-1997
 C:Accession: A35997
 R:Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
 A>Title: Rapid cloning of HLA-B cDNA by using the polymerase chain reaction: frequency
 A:Reference number: A35997; MUID:90207291; PMID:2320591
 A:Accession: A35997
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-364 <ENR>
 A:Cross-references: GB:M32321
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:219-284/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 34; DB 2; Length 364;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLYY 11
 DB 99 RSLRLALRY 109

RESULT 8
 T22251
 hypothetical protein F45H1.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T22251
 R:Kelly, P.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19537
 A:Accession: T22251
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-743 <MLB>
 A:Cross-references: EMBL:Z79420; PIDN:CAM01710.1; GSPDB:GN00019; CESP:F45H1.3
 A:Experimental source: clone F45H11
 C:Genetics:
 A:Gene: CESP:F45H1.3
 A:Map position: 1
 A:Introns: 28/3; 46/3; 82/1; 113/3; 250/1; 333/3; 355/3; 405/1; 498/2; 668/3; 701/1; 718
 C:Superfamily: Caenorhabditis elegans hypothetical protein F45H1.3

Query Match 60.7%; Score 34; DB 2; Length 743;
 Best Local Similarity 50.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXLRRLXLYY 12
 DB 696 RTRRLASTYY 707

RESULT 9
 T04435
 hypothetical protein T18B16.110 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Sep-1999
 C:Accession: T04435
 R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15359
 A:Accession: T04435
 A:Molecule type: DNA
 A:Residues: 1-253 <BEV>
 A:Cross-references: EMBL:AL021687
 A:Experimental source: cultivar Columbia; BAC clone T18B16
 C:Genetics:
 A:Map position: 4
 A:Introns: 70/3; 112/3; 155/2
 A>Note: T18B16.110

C:Superfamily: Arabidopsis hypothetical protein T18B16.110

Query Match 58.9%; Score 33; DB 2; Length 253;
 Best Local Similarity 42.9%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RXLRRLXLYY 14
 DB 53 RDKFRCDYVWAS 66

RESULT 10
 I38509
 MHC class I histocompatibility antigen - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jan-2000
 C:Accession: I38509
 R:Cereb, N.; Choi, J.W.; Rin, K.Z.; Yang, S.Y.
 Tissue Antigens 44, 271-273, 1994
 A>Title: HLA-B*5105, a newly identified B51 IEF variant.
 A:Reference number: I38509; MUID:95176331; PMID:7871530
 A:Accession: I38509
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-273 <RES>
 A:Cross-references: EMBL:U06697; NID:G469544; PIDN:AAA92997.1; PID:G469545
 C:Genetics:
 A:Gene: GDB:HLA-B
 A:Cross-references: GDB:120048; OMIM:142830
 A:Map position: 6p21.3-6p21.3
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:195-260/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 273;
 Best Local Similarity 63.6%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLYY 11
 DB 74 RNLRLALRY 84

RESULT 11
 I54463
 MHC HLA-B38 chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
 C:Accession: I54463
 R:Mueller, C.A.; Engler-Bloom, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
 Immunogenetics 30, 200-207, 1989
 A>Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificities
 A:Reference number: I54463; MUID:89379286; PMID:2777338
 A:Accession: I54463
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-274 <RES>
 A:Cross-references: GB:M29864; NID:G187674; PIDN:AAA36222.1; PID:G187675
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 274;
 Best Local Similarity 63.6%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLYY 11
 DB 75 RNLRLALRY 85

RESULT 12
 I59308
 class I histocompatibility antigen - pygmy chimpanzee (fragment)
 C:Species: Pan paniscus (pygmy chimpanzee, bonobo)

C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
 C/Accession: 159308
 R/McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
 Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
 A>Title: A uniquely high level of recombination at the HLA-B locus.
 A/Reference number: 159308; PMID:94286544; PMID:8016085
 A/Accession: 159308
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-354 <RES>
 A/Cross-references: EMBL:U05575; NID:g454767; PIDN:AAA50178.1; PID:g454768
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 354;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRXLXYY 11
 Db 91 RENTRIALRY 101

RESULT 13
 180167
 class I histocompatibility antigen - pygmy chimpanzee (fragment)
 C/Species: Pan paniscus (pygmy chimpanzee, bonobo)
 C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
 C/Accession: 180167
 R/McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
 Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
 A>Title: A uniquely high level of recombination at the HLA-B locus.
 A/Reference number: 159308; PMID:94286544; PMID:8016085
 A/Accession: 180167
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-354 <RES>
 A/Cross-references: EMBL:U05578; NID:g454773; PIDN:AAA50181.1; PID:g454774
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 354;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRXLXYY 11
 Db 91 RENTRIALRY 101

RESULT 14
 180169
 class I histocompatibility antigen - chimpanzee (fragment)
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
 C/Accession: 180169
 R/McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
 Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
 A>Title: A uniquely high level of recombination at the HLA-B locus.
 A/Reference number: 159308; PMID:94286544; PMID:8016085
 A/Accession: 180169
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-355 <RES>
 A/Cross-references: EMBL:U05580; NID:g454777; PIDN:AAA50183.1; PID:g454778
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 355;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRXLXYY 11

Db 91 RENTRIALRY 101

RESULT 15
 180171
 class I histocompatibility antigen - chimpanzee (fragment)
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jan-2000
 C/Accession: 180171
 R/McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
 Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
 A>Title: A uniquely high level of recombination at the HLA-B locus.
 A/Reference number: 159308; PMID:94286544; PMID:8016085
 A/Accession: 180171
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-355 <RES>
 A/Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 33; DB 2; Length 355;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRXLXYY 11
 Db 91 RENTRIALRY 101

Search completed: May 5, 2003, 14:03:02.
 Job time: 16 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 13:58:05 / Search time 25 Seconds
(without alignments)
23.227 Million cell updates/sec

Title: US-09-742-148A-3
Perfect score: 56
Sequence: 1 RXLRRLXLYYXWS 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	62.5	93	1 SY22_HUMAN	O00626 homo sapien
2	34	60.7	131	1 YGDD_ECOLI	P32065 escherichia
3	34	60.7	365	1 1A25_HUMAN	P18462 homo sapien
4	34	60.7	365	1 1A32_HUMAN	P10314 homo sapien
5	33	58.9	296	1 U007_HSV2H	P88430 herpes simp
6	33	58.9	359	1 1B01_PANTR	P13750 pan troglod
7	33	58.9	362	1 1B01_GORGO	P30379 gorilla gor
8	33	58.9	362	1 1B02_GORGO	P30380 gorilla gor
9	33	58.9	362	1 1B03_GORGO	P30381 gorilla gor
10	33	58.9	362	1 1B15_HUMAN	P10317 homo sapien
11	33	58.9	362	1 1B47_HUMAN	P10487 homo sapien
12	33	58.9	362	1 1B49_HUMAN	P14464 homo sapien
13	33	58.9	362	1 1B52_HUMAN	P30489 homo sapien
14	33	58.9	362	1 1B53_HUMAN	P30490 homo sapien
15	33	58.9	362	1 1B54_HUMAN	P30491 homo sapien
16	33	58.9	362	1 1B60_HUMAN	P18465 homo sapien
17	33	58.9	362	1 1B61_HUMAN	P30497 homo sapien
18	33	58.9	362	1 1B62_HUMAN	P10319 homo sapien
19	33	58.9	362	1 1B62_HUMAN	P10319 homo sapien
20	33	58.9	365	1 1A23_HUMAN	P30477 homo sapien
21	33	58.9	365	1 1A24_HUMAN	P05534 homo sapien
22	32	57.1	218	1 Y1DX_ECOLI	P31461 escherichia
23	32	57.1	342	1 G1NA_ACEXY	P37696 acetobacter
24	32	57.1	545	1 E5TC_DROPS	P25725 drosophila
25	31	55.4	199	1 Y59J_METU	Q58016 methanococ
26	31	55.4	162	1 G1NA_PSEFL	P10476 pseudomonas
27	31	55.4	3084	1 1NA4_MOUSE	P13137 mus musculu
28	30	53.6	186	1 1NA4_MOUSE	P07351 mus musculu
29	30	53.6	340	1 U120_HOMVA	P16758 human cytom
30	30	53.6	365	1 1A04_GORGO	P30378 gorilla gor
31	30	53.6	511	1 A1M5_MOUSE	P00687 mus musculu
32	30	53.6	549	1 LEM2_RAT	P98105 ratius norv
33	30	53.6	549	1 TRRF_ECOLI	P37196 escherichia

34	30	53.6	881	1 HELI_HSV2H	P28277 herpes simp
35	30	53.6	882	1 HELI_HSV1	P10189 herpes simp
36	30	53.6	1279	1 BCSG_PSEFL	P58937 pseudomonas
37	30	53.6	2048	1 RRP1_SENDE	P06829 sendai viru
38	30	53.6	2228	1 RRP1_SENDS	P27566 sendai viru
39	30	53.6	2228	1 RRP1_SENDF	P06996 sendai viru
40	30	53.6	2228	1 RRP1_SEND2	P16447 sendai viru
41	30	53.6	2233	1 RRP1_P13H4	P12577 human parai
42	29	51.8	125	1 YHFY_HAEIN	P44003 haemophilus
43	29	51.8	128	1 G1BO_MYCLE	O9cc59 mycobacteri
44	29	51.8	128	1 G1BO_MYCTU	O53197 mycobacteri
45	29	51.8	192	1 CD3E_SHBEP	P29328 ovais aries

ALIGNMENTS

RESULT 1
SY22_HUMAN STANDARD; PRT; 93 AA.
ID SY22_HUMAN
AC O00626;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A22 precursor (CC122) (Macrophage-derived chemokine) (stimulated T cell chemotactic protein 1) (CC chemokine SDCP-1).
DE SCVA22 OR MDC OR A-152E5.1.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-35.
RC TISSUE=Macrophage;
RX MEDLINE=97296313; PubMed=9151897;
RA Godiska R., Chantry D., Raport C.J., Sozzani S., Allavena P., Leyten D., Mantovani A., Gray P.W.;
RT "Human macrophage-derived chemokine (MDC), a novel chemotactant for monocytes, monocyte-derived dendritic cells, and natural killer cells.";
RL J. Exp. Med. 185:1595-1604(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=97460118; PubMed=9312138;
RA Chang M.-S., McNinch J., Elise C. III, Manthey C.L., Grosshans D., Meng T., Boone T., Andrew D.P.;
RT "Molecular cloning and functional characterization of a novel CC chemokine, stimulated T cell chemotactic protein (STCP-1) that specifically acts on activated T lymphocytes.";
RL J. Biol. Chem. 272:25229-25237(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Pulman J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=pancreas, and Spleen;
RA Straussberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP RECEPTOR INTERACTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R., Yoshie O., Gray P.W.;
RT "Macrophage-derived chemokine is a functional ligand for the CC

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RT Chemokine receptor 4.1;
RL J. Biol. Chem. 273:1764-1768(1998).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE TRAFFICKING OF ACTIVATED/EFFECTOR
CC T LYMPHOCYTES TO INFLAMMATORY SITES AND OTHER ASPECTS OF ACTIVATED
CC T LYMPHOCYTE PHYSIOLOGY. CHEMOTACTIC FOR MONOCYTES, DENDRITIC
CC CELLS AND NATURAL KILLER CELLS. MILD CHEMOATTRACTANT FOR PRIMARY
CC ACTIVATED T LYMPHOCYTES AND A POTENT CHEMOATTRACTANT FOR
CC CHRONICALLY ACTIVATED T LYMPHOCYTES BUT HAS NO CHEMOATTRACTANT
CC ACTIVITY FOR NEUTROPHILS, EOSINOPHILS, AND RESTING T LYMPHOCYTES.
CC BINDS TO CCR4.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN MACROPHAGE AND IN
CC MONOCYTE-DERIVED DENDRITIC CELLS, AND THYMUS. ALSO FOUND IN LYMPH
CC NODE, APPENDIX, ACTIVATED MONOCYTES, RESTING AND ACTIVATED
CC MACROPHAGES. LOWER EXPRESSION IN LUNG AND SPLEEN. VERY WEAK
CC EXPRESSION IN SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE INTERCINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL; U83171; AAB58360.1; -
DR EMBL; U83239; AAB53372.1; -
DR EMBL; AC004382; AAC24306.1; -
DR EMBL; BC027952; AAH27952.1; -
DR HSSP; G98157; 1CM9.
DR Genew; HGNC:10621; SCYA22.
DR MIM; 602957; -
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
DR KMW Cytokine; Chemotaxis; Signal.
FT CHAIN 1 24
FT DISULFID 25 93 SMALL INDUCIBLE CYTOKINE A22.
FT DISULFID 36 60 BY SIMILARITY.
FT DISULFID 37 76 BY SIMILARITY.
SQ SEQUENCE 93 AA; 10580 MW; 631FBE9CC083F787 CRC64;
Query Match 62.5%; Score 35; DB 1; Length 93;
Best Local Similarity 42.9%; Pred. No. 2.6;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RXLRLXLYYMXS 14
DB 44 RLPLRVKHFYWT 57
RESULT 2
ID YGDD_ECOLI STANDARD; PRT; 131 AA.
AC P32065;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Annotation update)
DE Hypothetical protein ygdD.
GN YGDD OR B2807 OR 24124 OR ECS3667.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562, 83334;
OX NCI_TaxID=562, 83334;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=955219098; PubMed=7704273;

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RA Everett M.J., Walsh T., Guay G., Bennett P.M.;
RT "GcYA, a lysr-type transcriptional regulator protein, activates
RT expression of the cloned citrobacter freundii ampc beta-lactamase
RT gene in Escherichia coli: cross-talk between DNA-binding proteins.";
RL Microbiology 141:419-430(1995).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426517; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL93 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postfai G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YGDD (E.COLI) / YWCK (IPA-61D)
CC (B.SUBTILIS) FAMILY.
CC -----
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CC -----
DR EMBL; X73413; CAA51814.1; -
DR EMBL; U29581; AAB40457.1; -
DR EMBL; AE000364; AAC75848.1; -
DR EMBL; AE005508; AAG57921.1; -
DR EMBL; AP002563; BAB37090.1; -
DR PIR; S34372; S34372.
DR Ecocore; EGI1793; ygdD.
GN Hypothetical protein; Transmembrane; Complete proteome.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562, 83334;
OX NCI_TaxID=562, 83334;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=955219098; PubMed=7704273;

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Query Match 60.7%; Score 34; DB 1; Length 131;
Best Local Similarity 50.0%; Pred. No. 5.7;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 RXLRLXLYYMXS 14
DB 64 RLISLWYWTGS 73
RESULT 3

```

1A25 HUMAN STANDARD; PRT; 365 AA.
 AC P18462; 095362;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class I histocompatibility antigen, A-25(A-10) alpha chain precursor.
 GN HLA-A OR HLA-A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (A*2501).
 RX MEDLINE=90207291; PubMed=2320591;
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
 RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency and nature of errors produced in amplification."; Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RL [2]
 RN SEQUENCE FROM N.A. (A*2502).
 RC TISSUE=hematopoietic;
 RX MEDLINE=97045042; PubMed=8881046;
 RA Krausa P., Young D.M., Gotch F.;
 RT "Identification of a new HLA-A allele (A*2502) by PCR-SSP."; Immunogenetics 45:84-85(1996).
 RL [1]
 RN IMMUNOGENETICS: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF A-25 ARE KNOWN: A*2501 AND A*2502. THE SEQUENCE SHOWN IS THAT OF A*2501.
 CC -----
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 CC -----
 DR EMBL; M32321; AAA63234.1; -
 DR EMBL; X97802; CAA63389.1; -
 DR PIR; A35997; A35997.
 DR HSP; 019673; 1HSB.
 DR MIM; 142800; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IGc1_1.
 DR PROSITE; PS00290; IG_MHC_1.
 DR MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 365
 FT
 FT DOMAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT DOMAIN 115 114 A-25(A-10) ALPHA CHAIN.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.
 FT DOMAIN 333 365 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 94 H -> O (IN A*2502).
 FT
 FT SEQUENCE 365 AA; 41218 MW; 00F71B2F97C3620 CRC64;
 SO
 Query Match 60.7%; Score 34; DB 1; Length 365;

Best Local Similarity 63.6%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RXLRRLXLY 11
 DB 99 RESRLRLRY 109
 RESULT 4
 ID 1A32 HUMAN STANDARD; PRT; 365 AA.
 AC P10314; Q29838;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class I histocompatibility antigen, A-32(AW-19) alpha chain precursor.
 GN HLA-A OR HLA-A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (A*3201).
 RA Domana J.D.;
 RT Submitted (DEC-1993) to the EMBL/Genbank/DBJ databases.
 RL [2]
 RN SEQUENCE OF 25-298 FROM N.A. (A*3201).
 RX MEDLINE=87058961; PubMed=2431040;
 RA Wan A.M., Ennis P., Parham P., Holmes N.;
 RT "The primary structure of HLA-A32 suggests a region involved in formation of the Bw4/Bw6 epitopes."; J. Immunol. 137:3671-3674(1986).
 RL [3]
 RN SEQUENCE FROM N.A. (A*3202).
 RC TISSUE=Blood;
 RX MEDLINE=97045038; PubMed=8881042;
 RA Zino E., Severini G.M., Mazzi B., Bordignon C., Benazzi E., Pleischauer K.;
 RT "Sequencing of a new HLA-A*32 subtype (A*3202)."; Immunogenetics 45:76-77(1996).
 RL [1]
 RN IMMUNOGENETICS: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF A-32 ARE KNOWN: A*3201 AND A*3202. THE SEQUENCE SHOWN IS THAT OF A*3201.
 CC -----
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 CC -----
 DR EMBL; U03907; AAA03605.1; -
 DR EMBL; X97120; CAA65786.1; -
 DR PIR; A26088; HLH032.
 DR HSP; 095352; 1HRK.
 DR MIM; 142800; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IGc1_1.
 DR PROSITE; PS00290; IG_MHC_1.
 DR MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 365
 FT
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT A-32(AW-19) ALPHA CHAIN.

FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 365 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 R -> H (IN A*3202).
 FT VARIANT 175 175 /FTID=VAR_004373.
 FT VARIANT 180 180 L -> Q (IN A*3202).
 FT VARIANT 180 180 /FTID=VAR_004374.
 FT SEQUENCE 365 AA; 41048 MW; BF7AF225329E0319 CRC64;
 SQ

Query Match 60.7%; Score 34; DB 1; Length 365;
 Best Local Similarity 63.6%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXLRXLYXYY 11
 Db 99 RESLRRLRY 109

RESULT 5
 UL07_HSV2H STANDARD; PRT; 296 AA.
 AC P89430;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein UL7.
 GN UL7.
 OS Herpes simplex virus (type 2 / strain HG52).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCB1_TaxID=10315;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Dolan A.;
 CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL7,
 CC BHV-1 55, VZV 53, EBV BBRF2, HCMV UL103 AND HSV-1 42.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; 286099; CAB06767.1;
 DR InterPro: IPR002600; Herpes UL7.
 DR Pfam: PF01677; Herpes_UL7; 1.
 SQ SEQUENCE 296 AA; 32967 MW; 4954AE449FF04024 CRC64;
 SQ

Query Match 58.9%; Score 33; DB 1; Length 296;
 Best Local Similarity 54.5%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRXLXYYXYS 14
 Db 271 LRSLVYWMWS 281

RESULT 6
 ID 1B01_PANTR STANDARD; PRT; 359 AA.
 AC P13750;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)

DE CHLA class I histocompatibility antigen, B-1 alpha chain precursor
 OS (Fragment).
 DE Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCB1_TaxID=9598;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89030641; PubMed=2460344;
 RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
 RA Klein J.;
 RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
 RT trans-species mode of evolution."
 RL EMBO J. 7:2765-2774(1988).
 RN [2]
 RP REVISIONS.
 RA Mayer W.;
 RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X13115; CAA31507.1;
 DR PIR; S03537; S03537.
 DR HSSP; P03989; IHSR.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00129; MHC_I; 1.
 DR Prodom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGc1_1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 KM NON_TER
 FT SIGNAL 1
 FT CHAIN 21 359
 FT -----
 FT DOMAIN 21 110 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT DOMAIN 111 202 B-1 ALPHA CHAIN.
 FT DOMAIN 203 294 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 295 305 EXTRACELLULAR ALPHA-2.
 FT TRANSMEM 306 329 CONNECTING PEPTIDE.
 FT DOMAIN 330 359 CYTOPLASMIC TAIL.
 FT DISULFID 121 184 BY SIMILARITY.
 FT DISULFID 223 279 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 SQ SEQUENCE 359 AA; 40173 MW; 858ACBAF74D6829D CRC64;
 SQ

Query Match 58.9%; Score 33; DB 1; Length 359;
 Best Local Similarity 63.6%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXLRXLYXYY 11
 Db 95 RENTRLRLRY 105

RESULT 7
 ID 1B01_GORGO STANDARD; PRT; 362 AA.
 AC P30379;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

```

DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Class I histocompatibility antigen, GOGO-B0101 alpha chain precursor.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OK NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078860; PubMed=1744581;
RA Lawlor D.A., Warren E., Taylor P., Parham P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I."
J. Exp. Med. 174:1491-1509(1991).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; X60255; CAA42807.1; -
DR PIR; JH0539; JH0539.
DR HSP; P03989; IHSB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_I_1.
DR ProDom; PD000050; MHC_I_1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40170 MW; 419EE29817165A4 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXY 11
DB 99 RENVIRALRY 109

RESULT 8
1B02_GORGO STANDARD; PRT; 362 AA.
AC P30380;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Class I histocompatibility antigen, GOGO-B0102 alpha chain precursor.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OK NCBI_TaxID=9595;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078860; PubMed=1744581;
RA Lawlor D.A., Warren E., Taylor P., Parham P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I."
J. Exp. Med. 174:1491-1509(1991).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; X60693; CAA43101.1; -
DR PIR; JH0540; JH0540.
DR HSP; P03989; IHSB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_I_1.
DR ProDom; PD000050; MHC_I_1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40204 MW; E19EE2B7C7BCD CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXY 11
DB 99 RENVIRALRY 109

RESULT 9
1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Class I histocompatibility antigen, GOGO-B0103 alpha chain precursor.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OK NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078860; PubMed=1744581;
RA Lawlor D.A., Warren E., Taylor P., Parham P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I."

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RL J. Exp. Med. 174:1491-1509(1991).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
CC EMBL; X60254; CAA42806.1; -
CC PIR; JH0541; JH0541.
CC HSSP; P03989; ILSA.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003597; IG_cl.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I; 1.
CC ProDom; PD000050; MHC_I; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC_I; Transmembrane; Glycoprotein; Signal.
CC SIGNL 1 24
CC CHAIN 25 362
CC -----
CC CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC GOGO-B0103 ALPHA CHAIN.
CC DOMAIN 25 114
CC FT 115 206
CC FT 207 298
CC FT 299 308
CC TRANSMEM 309 332
CC FT 333 362
CC FT 125 188
CC FT 227 283
CC DISULFID 227 283
CC CARBOHYD 110 110
CC SEQUENCE 362 AA; 40248 MW; 3DEB82572BD81469 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRILXYY 11
Db 99 RENTRIALRY 109

RESULT 10
ID 1B15 HUMAN STANDARD; PRT; 362 AA.
AC P10317;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B-27 B*2702 alpha chain
DE precursor (B-27K) (B27.2).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid:9606;
OX (1)
RN RP SEQUENCE FROM N.A.
RX MEDLINE=86220133; PubMed=3011411;
RT Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;
RT "Gene conversion-like mechanisms may generate polymorphism in human
RT class I genes.";
RL EMBL J. 5:547-552(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96086486; PubMed=7482496;

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RA Moses J.H., Marsh S.G., Arnett K.L., Adams E.J., Bodmer J.G.,
RA Parham P.;
RA "On the nucleotide sequences of B*2702 and B*2705.";
RA Tissue Antigens 46:50-53(1995).
RL [3]
RN RP SEQUENCE OF 86-107 AND 171-181.
RX MEDLINE=86042671; PubMed=2414775;
RA Vega M.A., Ezquerro A., Rojo S., Aparicio P., Bragado R.,
RA Lopez de Castro J.A.;
RT "Structural analysis of an HLA-B*27 functional variant: identification
RT of residues that contribute to the specificity of recognition by
RT cytolytic T lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
CC EMBL; X03664; CAA7301.1; -
CC EMBL; X03667; CAA7301.1; JOINED.
CC EMBL; L28504; AAA69724.1; -
CC PIR; B25092; HLHDBK.
CC HSSP; P03989; ILSA.
CC MIM; 142830; -
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003597; IG_cl.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I; 1.
CC ProDom; PD000050; MHC_I; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC_I; Transmembrane; Glycoprotein; Signal.
CC SIGNL 1 24
CC CHAIN 25 362
CC -----
CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC B-27 B*2702 ALPHA CHAIN.
CC DOMAIN 25 114
CC FT 115 206
CC FT 207 298
CC FT 299 308
CC TRANSMEM 309 332
CC FT 333 362
CC FT 125 110
CC FT 110 110
CC FT 125 188
CC FT 227 283
CC DISULFID 227 283
CC SEQUENCE 362 AA; 40397 MW; C8D5A72ED32E2F88 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRILXYY 11
Db 99 RENTRIALRY 109

RESULT 11
ID 1B47 HUMAN STANDARD; PRT; 362 AA.
AC P30487;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B-49(B*21) B*4901 alpha chain
DE precursor.

```


GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89305215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP REVISION TO 78.
 RA MEDLINE=93056529; PubMed=1385528;
 RA Hildebrand W.H., Madrigal J.A., Belich M.P., Zemmour J., Ward F.E.,
 RA Williams R.C., Parham P.;
 RT "Serologic cross-reactivities poorly reflect allelic relationships in
 the HLA-B*2 and HLA-B*1 groups. Dominant epitopes of the alpha 2
 helix."
 RL J. Immunol. 149:3563-3568(1992).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----
 DR EMBL: M24037; AAA02950.1; -
 DR HSSP: P30491; LAIO.
 DR MIM: 142830; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; IG_1.
 DR Pfam: PF00129; MHC_I; 1.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IG1; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT FT 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 188
 FT DISULFID 125 158
 FT DISULFID 227 283
 SO SEQUENCE 362 AA; 40581 MW; 77B1C82AD3DAE54A CRC64;
 Query Match 58.9%; Score 33; DB 1; Length 362;
 Best Local Similarity 63.6%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RXLRXLY 11
 DB 99 RENTRLRY 109
 RESULT 12
 ID 1B49 HUMAN STANDARD; PRT; 362 AA.
 AC P18464;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class I histocompatibility antigen, B-51(B-5) B*5101 alpha chain
 DE precursor.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90207291; PubMed=2220591;
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
 RT "Rapid cloning of HLA-A,B,C DNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89080265; PubMed=2909619;
 RA Hayashi H., Ennis P.D., Ariga H., Salter R.D., Parham P., Kano K.,
 RA Takiguchi M.;
 RT "HLA-B*1 and HLA-B*52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain."
 RL J. Immunol. 142:306-311(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89233295; PubMed=2714852;
 RA Pohl H., Kuon W., Tabaczewski P., Doerner C., Weiss B.H.;
 RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
 RT the HLA-B alleles."
 RL Immunogenetics 29:297-307(1989).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----
 DR EMBL: M32319; AAA56232.1; -
 DR EMBL: M22782; AAA59620.1; ALT_SEQ.
 DR EMBL: M22786; AAA59620.1; JOINED.
 DR EMBL: M22787; AAA59620.1; JOINED.
 DR EMBL: M22788; AAA59620.1; JOINED.
 DR EMBL: M22789; AAA59620.1; JOINED.
 DR EMBL: M22790; AAA59620.1; JOINED.
 DR EMBL: M22791; AAA59620.1; JOINED.
 DR EMBL: L41087; AAA64513.1; -
 DR EMBL: L41086; AAA64513.1; JOINED.
 DR PIR: A30345; A30345.
 DR PIR: A30548; A30548.
 DR HSSP: P30491; LAIO.
 DR MIM: 142830; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; IG_1.
 DR Pfam: PF00129; MHC_I; 1.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IG1; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT FT 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-51(B-5) B*5101 ALPHA CHAIN.
 EXTRACELLULAR ALPHA-1.
 EXTRACELLULAR ALPHA-2.
 EXTRACELLULAR ALPHA-3.

```
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 110 110
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40566 MW; D104163B4CC71F92 CRC64;

Query Match
Best Local Similarity 58.9%; Score 33; DB 1; Length 362;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 99 RENTRILRY 109

RESULT 13
ID 1B52 HUMAN STANDARD; PRT; 362 AA.
AC P30489;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, B*5104 alpha chain
DE precursor.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92269955; PubMed=1317015;
RA Bellch M.P., Madrigal J.A., Hildebrand W.H., Zemmour J.,
RA Williams R.C., Luz R., Petzl-Erler M.L., Parham P.;
RT "Unusual HLA-B alleles in two tribes of Brazilian Indians.";
RL Nature 357:326-329(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z15143; CAA78849.1;
CC HSSP; P30491; 1A10.
CC MIM; 142830;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_I.
DR Pfam; PF00050; MHC_I.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT 115 114 B*5104 ALPHA CHAIN.
FT 207 298 EXTRACELLULAR ALPHA-1.
FT 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
```

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FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40560 MW; 1DF5247796583B08 CRC64;

Query Match
Best Local Similarity 58.9%; Score 33; DB 1; Length 362;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 99 RENTRILRY 109

RESULT 14
ID 1B53 HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, BW*5201 alpha chain
DE precursor.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89080265; PubMed=2909619;
RA Hayashi H., Ennis P.D., Ariga H., Salter R.D., Parham P., Kano K.,
RA Takiguchi M.;
RT "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
RT helical region of the alpha 1 domain.";
RL J. Immunol. 142:306-311(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M22799; AAA59645.1; ALT SEQ.
CC EMBL; M22793; AAA59645.1; JOINED.
CC EMBL; M22794; AAA59645.1; JOINED.
CC EMBL; M22795; AAA59645.1; JOINED.
CC EMBL; M22796; AAA59645.1; JOINED.
CC EMBL; M22797; AAA59645.1; JOINED.
CC EMBL; M22798; AAA59645.1; JOINED.
CC PIR; B30345; B30345.
CC PIR; B30548; B30548.
CC HSSP; P30491; 1A10.
CC MIM; 142830;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00129; MHC_I.
DR Pfam; PF00050; MHC_I.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT 115 114 BW*5201 ALPHA CHAIN.
FT 206 206 EXTRACELLULAR ALPHA-1.
FT 206 206 EXTRACELLULAR ALPHA-2.
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FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 160 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40521 MW; A3E36370FD84F91 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRIXLXY 11
Db 99 RENTRIALRY 109

RESULT 15
ID 1B54 HUMAN STANDARD; PRT: 362 AA.
AC P30451.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, BW-53 B*5301 alpha chain
DE precursor.
CN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91033941; PubMed=1699887;
RA Hayashi H., Ooba T., Nakayama S., Sekimata M., Kano K.,
RA Takiguchi M.;
RT "Allospecificities between HLA-Bw53 and HLA-B35 are generated by
RT substitution of the residues associated with HLA-Bw4/Bw6 public
RT epitopes."
RL Immunogenetics 32:195-199(1990).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
RP MEDLINE=96209672; PubMed=8624812;
RA Smith K.J., Reid S.W., Harlos K., McMichael A.J., Stuart D.I.,
RA Bell J.I., Jones E.Y.;
RT "Bound water structure and polymorphic amino acids act together to
RT allow the binding of different peptides to MHC class I HLA-B53."
RL Immunity 4:215-228(1996).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, M58636; AAA36228.1; -
CC PIR, A45834; A45834.
CC PDB, 1A1M; 08-APR-98.
CC PDB, 1A1O; 08-APR-98.
CC MIM, 142830; -
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003597; IG_C1.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; IG_1.
CC Pfam; PF00129; MHC_I; 1.
CC ProDom; PD000050; MHC_I; 1.
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DR SMART; SMO0407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KM MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 BW-53 B*5301 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT CARBOHYD 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40495 MW; 57BA74BD7854658 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 362;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RXXLRIXLXY 11
Db 99 RENTRIALRY 109

Search completed: May 5, 2003, 14:00:42
Job time : 26 secs
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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 13:59:05 ; Search time 28 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-742-148a-3
Perfect score: 56
Sequence: 1 RXLRXIXLYYXWS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	66.1	354	7	Q95528
2	36	64.3	59	13	O13145
3	36	64.3	284	2	P71511
4	34	60.7	131	2	Q46667
5	34	60.7	131	16	O8XEU8
6	34	60.7	181	7	O9TQGO
7	34	60.7	181	7	O9TQF9
8	34	60.7	181	7	O9TQF5
9	34	60.7	181	7	O9TQF3
10	34	60.7	181	7	O9TQF2
11	34	60.7	181	7	O9TQF8
12	34	60.7	181	7	O9TQF6
13	34	60.7	181	7	O9MYE9
14	34	60.7	181	7	O9BD43
15	34	60.7	181	7	O9UQ03
16	34	60.7	181	7	O95124

17	34	60.7	181	7	Q95122	Q95122 homo sapien
18	34	60.7	181	7	Q951E8	Q951E8 homo sapien
19	34	60.7	181	7	Q951D5	Q951D5 homo sapien
20	34	60.7	326	7	Q9GJ45	Q9GJ45 homo sapien
21	34	60.7	359	7	Q30595	Q30595 macaca mula
22	34	60.7	364	7	Q9GJ43	Q9GJ43 homo sapien
23	34	60.7	365	7	Q9MYG5	Q9MYG5 homo sapien
24	34	60.7	365	7	Q9GJ44	Q9GJ44 homo sapien
25	34	60.7	512	8	Q9MT01	Q9MT01 oenothera h
26	33	58.9	89	7	O19569	O19569 homo sapien
27	33	58.9	89	7	Q9UQ74	Q9UQ74 homo sapien
28	33	58.9	89	7	Q9UBX9	Q9UBX9 homo sapien
29	33	58.9	90	7	O46697	O46697 gorilla gor
30	33	58.9	133	7	O19189	O19189 homo sapien
31	33	58.9	138	7	O78209	O78209 homo sapien
32	33	58.9	142	7	Q951Z0	Q951Z0 homo sapien
33	33	58.9	172	7	O19780	O19780 homo sapien
34	33	58.9	172	7	O19770	O19770 homo sapien
35	33	58.9	172	7	O19774	O19774 homo sapien
36	33	58.9	172	7	O19775	O19775 homo sapien
37	33	58.9	172	7	O19771	O19771 homo sapien
38	33	58.9	172	7	O19772	O19772 homo sapien
39	33	58.9	172	7	O19773	O19773 homo sapien
40	33	58.9	172	7	Q95364	Q95364 homo sapien
41	33	58.9	175	7	Q29694	Q29694 homo sapien
42	33	58.9	175	7	O9TQE7	O9TQE7 homo sapien
43	33	58.9	176	7	O9BCM0	O9BCM0 homo sapien
44	33	58.9	180	7	O9TQK7	O9TQK7 homo sapien
45	33	58.9	180	7	O9TQK6	O9TQK6 homo sapien

ALIGNMENTS

RESULT 1
ID Q95528 PRELIMINARY: PRT; 354 AA.
AC Q95528;
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-UN-2002 (TREMBLrel. 21, Last annotation update)
DE Claes I histocompatibility antigen (fragment).
OS HLA-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94286544; PubMed=8016085;
RA McAdam S.N., Boyson J.E., Liu X., Garber T.L., Hughes A.L.,
RA Bontrop R.E., Watkins D.I.;
RT "A uniquely high level of recombination at the HLA-B locus";
RT Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; U05579; AAA50182.1; -;
CC HSSP; P03989; 1HSA.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003066; IG_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I_1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I_1.
DR SMART; SM00407; IGc1_1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 354 AA; 39539 MW; 353E85AD455A9EF1 CRC64;

Query Match 66.1%; Score 37; DB 7; Length 354;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RXXLRILXYWXS 14
DB 91 RENDRLRLRYFQS 104

RESULT 2

013145 PRELIMINARY; PRT; 59 AA.
AC 013145;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Carboxyl ester lipase (Fragment).
GN CELIP OR DANIO-CELIP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20576369; PubMed=11016933;
RA Bertrand C., Chabonnet A., Takke C., Yan Y., Postlethwait J.,
RT Tourant J.P., Cousin X.;
RT "Zebrafish Acetylcholinesterase Is Encoded by a Single Gene Localized
RT on Linkage Group 7, GENE STRUCTURE AND POLYMORPHISM; MOLECULAR FORMS
RT AND EXPRESSION PATTERN DURING DEVELOPMENT.";
RL J. Biol. Chem. 276:464-474(2001).
DR EMBL; AF003943; AAB61463.1; -
DR HSSP; P30122; 2BCE.
DR ZFIN; ZDB-GENE-990415-26; celip.
FT NON_TER 1 1
SQ SEQUENCE 59 AA; 6890 MW; D9DE43FD74D3364 CRC64;

Query Match 64.3%; Score 36; DB 13; Length 59;
Best Local Similarity 54.5%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRILXLYWXS 14
DB 39 LRRLVYWT 49

RESULT 3

0171511 PRELIMINARY; PRT; 284 AA.
AC 0171511;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Mxau homolog.
GN Mxau.
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.

OK NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AM1;
RX MEDLINE=97312011; PubMed=9168622;
RA Chioresardova L., Lidstrom M.E.;
RT "Molecular and mutational analysis of a DNA region separating two
RT methyloctrophy gene clusters in Methylobacterium extorquens AM1.";
RL Microbiolgy 143:1729-1736(1997).
DR EMBL; U72662; AAB58892.1; -
DR InterPro; IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPB; 1.
SQ SEQUENCE 284 AA; 31032 MW; 0A3CBFEED3E09B6 CRC64;

Query Match 64.3%; Score 36; DB 2; Length 284;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRILXLYW 12
DB 69 LKVKLRYYW 77

RESULT 4

046667 PRELIMINARY; PRT; 131 AA.
AC 046667;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 14.3 kDa protein.
GN ORF2.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.

OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=94245611; PubMed=8188587;
RA Wilson R.L., Stauffer G.V.;
RT "DNA sequence and characterization of GcvA, a LysR family regulatory
RT protein for the Escherichia coli glycine cleavage enzyme system.";
RL J. Bacteriol. 176:2862-2868(1994).
DR EMBL; U01030; AAC13743.1; -
KM Hypothetical protein.
SQ SEQUENCE 131 AA; 14319 MW; C0EC023EA3FB722 CRC64;

Query Match 60.7%; Score 34; DB 2; Length 131;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 RILXLYWXS 14
DB 64 RISIMFYWXS 73

RESULT 5

08XEU8 PRELIMINARY; PRT; 131 AA.
AC 08XEU8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative small membrane protein (Hypothetical protein STY3121).
GN YGDP OR STW2981 OR STY3121.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.

OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvany E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston K., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S. typhi; STRAIN=CT18;

RA MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrer J.,
RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krog A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant *Salmonella*
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AE008836; AAL21859.1; -
DR EMBL; AL627277; CAD02807.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 131 AA; 1438 MW; E975B18231E18FA9 CRC64;

Query Match 60.7%; Score 34; DB 16; Length 131;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 RIXLXYMXS 14
DB 64 RISTWYWS 73

RESULT 6
Q9TQ60 PRELIMINARY; PRT; 181 AA.
ID Q9TQ60;
AC Q9TQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RA Ng J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF137076; AAD33737.1; -
DR HSSP; Q93352; 1HMK.
DR HSSP; Q93352; 1HMK.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21391 MW; 85801CDA270FC838 CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;
Best Local Similarity 63.6%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXLYXY 11
DB 74 RESLRALRY 84

RESULT 7
Q9TQ60 PRELIMINARY; PRT; 181 AA.
ID Q9TQ60;
AC Q9TQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RA Ng J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF137078; AAD33738.1; -
DR EMBL; AF137077; AAD33738.1; JOINED.
DR HSSP; O19673; 1TWC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21137 MW; 78B54FF20B00B7C CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;
Best Local Similarity 63.6%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXLYXY 11
DB 74 RESLRALRY 84

RESULT 8
Q9TQ60 PRELIMINARY; PRT; 181 AA.
ID Q9TQ60;
AC Q9TQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RA Ng J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF139892; AAD33849.1; -
DR EMBL; AF139891; AAD33849.1; JOINED.
DR HSSP; O19673; 1TWC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21137 MW; 78B54FF20B00B7C CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;
Best Local Similarity 63.6%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXLYXY 11
DB 74 RESLRALRY 84

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RESULT 9
Q9TF3 PRELIMINARY; PRT; 181 AA.
ID Q9TF3;
AC Q9TF3;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RT "Seventeen more novel HLA-A locus alleles."
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF140856; AAD34883.1; JOINED.
DR HSP; O19673; ITMC.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00129; MHC_I.1.
DR PRINTS; PR01638; MHCCLASSI.
DR Prodom; PD000050; MHC_I.1.
FT NON_TER 1 181
SQ SEQUENCE 181 AA; 21137 MW; 78B854FF20B087C CRC64;

Query Match
Best Local Similarity 60.7%; Score 34; DB 7; Length 181;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 74 RESLRALRY 84

RESULT 10
Q9TF2 PRELIMINARY; PRT; 181 AA.
ID Q9TF2;
AC Q9TF2;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RT "Seventeen more novel HLA-A locus alleles."
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF140857; AAD34884.1; JOINED.
DR HSP; O19673; ITMC.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00129; MHC_I.1.
DR PRINTS; PR01638; MHCCLASSI.
DR Prodom; PD000050; MHC_I.1.
FT NON_TER 1 181
SQ SEQUENCE 181 AA; 21137 MW; 78B854FF20B087C CRC64;

Query Match
Best Local Similarity 60.7%; Score 34; DB 7; Length 181;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 74 RESLRALRY 84

Query Match
Best Local Similarity 60.7%; Score 34; DB 7; Length 181;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 74 RESLRALRY 84

RESULT 11
Q9TF8 PRELIMINARY; PRT; 181 AA.
ID Q9TF8;
AC Q9TF8;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N., Kosman C., Henson V., Milton W., Koester R.,
RT "Seventeen more novel HLA-A locus alleles."
RL Tissue Antigens 55:369-373(2000).
DR EMBL; AF148897; AAD34010.1; JOINED.
DR HSP; Q95352; IHRK.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00129; MHC_I.1.
DR PRINTS; PR01638; MHCCLASSI.
DR Prodom; PD000050; MHC_I.1.
FT NON_TER 1 181
SQ SEQUENCE 181 AA; 21391 MW; 85601CDA270FCE38 CRC64;

Query Match
Best Local Similarity 60.7%; Score 34; DB 7; Length 181;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXXY 11
DB 74 RESLRALRY 84

RESULT 12
Q9TF6 PRELIMINARY; PRT; 181 AA.
ID Q9TF6;
AC Q9TF6;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jones P.F., Hurley C.K.;
RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF198653; AAF20814.1; JOINED.
DR EMBL; AF198652; AAF20814.1; JOINED.
DR HSP; P30685; IASB.
DR InterPro; IPR01039; MHC_I.
DR Pfam; PF00129; MHC_I.1.
DR PRINTS; PR01638; MHCCLASSI.
DR Prodom; PD000050; MHC_I.1.
FT NON_TER 1 181
SQ SEQUENCE 181 AA; 21391 MW; 85601CDA270FCE38 CRC64;
```


SQ SEQUENCE 181 AA; 21045 MW; 917EC21D3DA3B085 CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;

Best Local Similarity 63.6%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXLYY 11
| | | | |
74 RESLRIALRY 84

RESULT 13

ID Q9MYE9 PRELIMINARY; PRT; 181 AA.

AC Q9MYE9; 09MYE9;

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE MHC class I antigen (Fragment).

GN HLA-A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCB1_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Jones P.F., Hurley C.K.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF226837; AAF29554.1; -

DR EMBL; AF226836; AAF29554.1; JOINED.

DR HSSP; Q95352; 1HK.

DR InterPro; IPR001039; MHC_I.

DR Pfam; PF00129; MHC_I.1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC_I.1.

FT NON_TER 1 181

FT NON_TER 1 181

SQ SEQUENCE 181 AA; 21087 MW; 310607892ACD02E2 CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;

Best Local Similarity 63.6%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXLYY 11
| | | | |
74 RESLRIALRY 84

RESULT 14

ID Q9BD43 PRELIMINARY; PRT; 181 AA.

AC Q9BD43; 09BD43;

DT 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE MHC class I antigen (Fragment).

GN HLA-B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCB1_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Tait B., Holdsworth R., Cantwell L., Boyle A., Diviney M.;

RT "Confirmatory B*5305 sequence."

Submited (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF304003; AAG53942.1; -

DR EMBL; AF304002; AAG53942.1; JOINED.

DR HSSP; P30685; 1A9B.

DR InterPro; IPR001039; MHC_I.

DR Pfam; PF00129; MHC_I.1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC_I.1.

FT NON_TER 1 1

FT NON_TER 1 181

SQ SEQUENCE 181 AA; 21045 MW; 917EC21D3DA3B085 CRC64;

QY 1 RXXLRXIXLYY 11
| | | | |
74 RESLRIALRY 84

RESULT 15

ID Q9U0U3 PRELIMINARY; PRT; 181 AA.

AC Q9U0U3; 09U0U3;

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DE Human leucocyte antigen A (Fragment).

GN HLA-A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCB1_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Guttridge M.G.;

RL "Sequence confirmation of HLA-A*2502."

DR EMBL; AJ238524; CAB41888.1; -

DR HSSP; O19673; 1TMC.

DR InterPro; IPR001039; MHC_I.

DR Pfam; PF00129; MHC_I.1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC_I.1.

FT NON_TER 1 181

FT NON_TER 1 181

SQ SEQUENCE 181 AA; 21398 MW; 1AAC96709AB73206 CRC64;

Query Match 60.7%; Score 34; DB 7; Length 181;

Best Local Similarity 63.6%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXXLRXIXLYY 11
| | | | |
74 RESLRIALRY 84

Search completed: May 5, 2003, 14:02:40
Job time : 29 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using bw model

Run on: May 5, 2003, 13:58:05 ; Search time 75 Seconds
(without alignments)
24.873 Million cell updates/sec

Title: US-09-742-148a-3
Perfect score: 56
Sequence: 1 RXLRRLXLYYXMS 14

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq_101002.*
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3: /SIDSz/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT.*
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5: /SIDSz/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT.*
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23: /SIDSz/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	82.1	14	17	AAW07511
2	46	82.1	14	22	AAW07511
3	41	73.2	10	22	AAW72482
4	41	73.2	10	22	AAW59457
5	41	73.2	14	22	AAW59417
6	41	73.2	14	22	AAW59418
7	37	66.1	83	22	AAW74879
8	35	62.5	13	22	AAW59419
9	35	62.5	37	22	ABB39053
10	35	62.5	37	22	AAW59705

11	35	62.5	37	22	AAW72285
12	35	62.5	37	22	AAW32544
13	35	62.5	37	23	ABG42100
14	35	62.5	68	18	AAW17668
15	35	62.5	69	18	AAW20061
16	35	62.5	69	20	AAW24415
17	35	62.5	69	20	AAW05874
18	35	62.5	69	23	AAW02022
19	35	62.5	69	23	AAW04155
20	35	62.5	70	18	AAW00060
21	35	62.5	70	20	AAW24413
22	35	62.5	70	20	AAW05873
23	35	62.5	86	19	AAW59432
24	35	62.5	93	18	AAW07604
25	35	62.5	93	18	AAW00058
26	35	62.5	93	18	AAW62783
27	35	62.5	93	19	AAW57881
28	35	62.5	93	19	AAW59433
29	35	62.5	93	19	AAW40811
30	35	62.5	93	20	AAW26175
31	35	62.5	93	20	AAW24414
32	35	62.5	93	20	AAW05879
33	35	62.5	93	20	AAW05880
34	35	62.5	93	20	AAW05871
35	35	62.5	93	20	AAW06829
36	35	62.5	93	21	AAW07500
37	35	62.5	93	22	AAW68352
38	35	62.5	93	23	AAW04046
39	35	62.5	154	20	AAW05878
40	35	62.5	172	20	AAW29895
41	35	62.5	334	20	AAW29904
42	35	62.5	587	20	AAW29900
43	33	58.9	79	22	AAW07472
44	33	58.9	79	22	AAW18309
45	33	58.9	79	22	AAW05915

ALIGNMENTS

RESULT 1	
AAW07511	
ID	AAW07511 standard; peptide; 14 AA.
AC	AAW07511;
DT	04-AUG-1997 (first entry)
DE	Generic T-cell modulating peptide #2.
XX	
XX	T-cell modulator; autoimmune disease; tissue destruction; alpha1-domain; mammal; major histocompatibility complex; MHC class I; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease; thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy;
XX	generic peptide.
OS	Synthetic.
XX	
FX	Key
FT	Misc-difference 2
FT	Misc-difference 7
FT	Misc-difference 9
FT	Misc-difference 13
FT	Misc-difference 13
XX	Label= Gln, Asp
XX	
PN	W09635443-Al.
PD	14-NOV-1996.

Human bone marrow
Peptide #6581 enco
Human peptide enco
Stem cell mobilist
Human macrophage d
Human macrophage d
Human macrophage-d
Human chemokine MD
Human MOC protein.
Human macrophage d
Macrophage derived
Human macrophage-d
Human chemokine pr
Cytokine beta-13 s
Macrophage derived
Amino acid sequenc
Human chemokine be
Human chemokine be
Macrophage-derived
Macrophage-derived
Human macrophage-d
Macaque macrophage
Human macrophage-d
Macrophage derived
A human monokine d
Amino acid sequenc
Human macrophage-d
Yeast pre-pro-alpha
Human MOC and huma
Human MOC and HIV-
Human bone marrow
Peptide #4743 enco
Peptide #4597 enco

XX 05-APR-1996; 96WO-US04710.
XX
XX 12-MAY-1995; 95US-0440504.
XX
XX (SANG-) SANGSTAT MEDICAL CORP.
XX
XX Buejow R;
XX
XX WPI; 1996-518410/51.
XX
XX Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset
PT of clinical symptoms of insulin dependent diabetes by modulating T
PT cell mediated attack on target cells
XX
XX
XX Claim 2: Page 20; 24pp; English.
XX
XX
XX AAW07510 and AAW07511 represent generic T-cell modulating peptides.
XX These sequences, and specific peptides created from them (such as
XX AAW07512-W07518) can be used in the method of the invention. The method
XX is for affecting the course of an autoimmune disease involving T-cell
XX mediated destruction of tissue in mammals. These sequences are based on
XX the alpha-domains of the major histocompatibility complex (MHC)
XX antigen. These peptides are used especially to treat insulin-dependent
XX diabetes mellitus, preferably being administered during the pre-clinical
XX stage to delay onset of the disease. Other diseases that can be treated
XX are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus
XX vulgaris, Sjogren's disease, thyroid disease, Hashimoto's thyroiditis,
XX myasthenia gravis, etc. The peptides modulate T-cell mediated attack on
XX autologous target cells, and may also reduce inflammation, swelling, and
XX release of cytokines, perforins, granzymes etc. associated with T cell
XX activation.
XX
SQ Sequence 14 AA;
Query Match 82.1%; Score 46; DB 17; Length 14;
Best Local Similarity 92.9%; Pred. No. 0.035;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RXKLRIKLYYWX 14
Db 1 RXBLRIKLYYWX 14
RESULT 2
AAB59403
ID AAB59403 standard; Peptide; 14 AA.
XX
XX AAB59403;
XX
XX 22-MAR-2001 (first entry)
XX
XX Human Class I HLA-B alpha1-domain-derived peptide #3.
XX
XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
XX cytotoxic T cell activation inhibition; cell transplantation;
XX natural killer cell activation inhibition; organ transplantation.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 2 /label= Val, Glu
XX FT Misc-difference 3 /label= Asn, Asp
XX FT Misc-difference 7 /label= Ala, Leu
XX FT Misc-difference 9 /label= Arg, Glu
XX FT Misc-difference 13 /label= Glu, Asp
XX FT

XX US6162434-A.
XX
XX 19-DEC-2000.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX (SANG-) SANGSTAT MEDICAL CORP.
XX
XX Buejow R;
XX
XX WPI; 2001-111720/12.
XX
XX
XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
XX
XX Claim 8; Column 37; 20pp; English.
XX
XX
XX The present sequence is a peptide which may be used in a method for
XX inhibiting activation of cytotoxic T lymphocytes and/or natural killer
XX cells. The method involves combining the cells with a compound
XX comprising an oligopeptide of at least 6 amino acids comprising a
XX contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
XX including amino acids 84-86, where amino acids 84-86 are YW.
XX
XX The method is useful for transplanting a donor mammalian organ or cells
XX to a mammalian recipient. The organ or cells are combined with the
XX compound prior to implanting in the mammalian recipient, or the compound
XX may be administered to the mammalian recipient in a period extending
XX from prior to implanting the donor organ or cells.
XX
SQ Sequence 14 AA;
Query Match 82.1%; Score 46; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXKLRIKLYYWX 14
Db 1 RXKLRIKLYYWX 14

RESULT 3
AAV72482
ID AAV72482 standard; peptide; 10 AA.
XX
XX AAV72482;
XX
XX 24-APR-2001 (first entry)
XX
XX Immunosuppressive peptide, P15, to prevent allograft rejection.
XX
XX Immunosuppressive; allograft rejection; topological parameter;
XX physico-chemical parameter; in silico screening; pharmaceutical;
XX cosmetic; agrochemical; biomaterial; veterinary application.
XX
XX Unidentified.
XX
XX WO200079263-A2.
XX
XX 28-DEC-2000.
XX
XX 15-MAY-2000; 2000WO-EP04338.
XX
XX 18-JUN-1999; 99EP-0401526.
XX
XX (SYNT-) SYNT:EM SA.
XX
XX Lahana R, Clair P, Yaseri A;
XX
XX WPI; 2001-091623/10.
XX
XX

XX Identifying active candidate molecules on the basis of selected
PT physico-chemical parameters, for in silico screening of compounds
PT useful in pharmaceuticals, cosmetics, veterinary applications and
PT agrochemicals
XX
PS Disclosure; Page 38; 55pp; English.
XX
CC The present invention relates to a method for identifying
CC physico-chemical and/or topological parameters associated with biological
CC activity. The method involves selecting the first subset from
CC predetermined set of physico-chemical parameters, determining their value
CC of function, and selecting the second subset from physico-chemical
CC parameters based on the values of function, such that each second subset
CC is more closely associated with the activity than the first subset. The
CC selected physico-chemical parameters are useful for developing criteria
CC for screening candidate molecules and are suitable for use in silico
CC screening of compounds. The compounds may be used in pharmaceuticals,
CC cosmetics, agrochemicals, biomaterials and in veterinary applications. It
CC is also useful as an antibiotic or antifungal agent. The present
CC sequence is an immunosuppressive peptide, P15, identified by in silico
CC screening. The immunosuppressive activity of the peptide that prevents
CC allograft rejection is tested in a heterotopic allograft model of mouse.
XX
SQ Sequence 10 AA;
XX
Query Match 73.2%; Score 41; DB 22; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 LRILXLYYW 12
DB 2 LRILRYW 10
XX
RESULT 4
AAB59457
ID AAB59457 standard; Peptide; 10 AA.
XX
AC AAB59457;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human Class I HLA-B alpha1-domain-derived peptide #57.
XX
KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
KW cytotoxic T cell activation inhibition; cell transplantation;
KW natural killer cell activation inhibition; organ transplantation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6162434-A.
XX
PD 19-DEC-2000.
XX
PF 03-MAY-1995; 95US-0433613.
XX
PR 03-MAY-1995; 95US-0433613.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R;
XX
DR WPI; 2001-111720/12.
XX
PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
PS Claim 12; Column 38; 20pp; English.
XX
CC The present sequence is a peptide which may be used in a method for

CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
CC cells. The method involves combining the cells with a compound
CC comprising an oligopeptide of at least 6 amino acids comprising a
CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
CC including amino acids 84-86, where amino acids 84-86 are YW.
CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.
XX
SQ Sequence 10 AA;
XX
Query Match 73.2%; Score 41; DB 22; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 LRILXLYYW 12
DB 2 LRILRYW 10
XX
RESULT 5
AAB59417
ID AAB59417 standard; Peptide; 14 AA.
XX
AC AAB59417;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human Class I HLA-B alpha1-domain-derived peptide #17.
XX
KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
KW cytotoxic T cell activation inhibition; cell transplantation;
KW natural killer cell activation inhibition; organ transplantation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6162434-A.
XX
PD 19-DEC-2000.
XX
PF 03-MAY-1995; 95US-0433613.
XX
PR 03-MAY-1995; 95US-0433613.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R;
XX
DR WPI; 2001-111720/12.
XX
PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
PS Disclosure; Column 7-8; 20pp; English.
XX
CC The present sequence is a peptide which may be used in a method for
CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
CC cells. The method involves combining the cells with a compound
CC comprising an oligopeptide of at least 6 amino acids comprising a
CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
CC including amino acids 84-86, where amino acids 84-86 are YW.
CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.
XX
SQ Sequence 14 AA;

Query Match 73.2%; Score 41; DB 22; Length 14;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIXLXYW 12
 |||||
 DB 6 LRIALRYW 14

RESULT 6
 AAB59418
 ID AAB59418 standard; Peptide; 14 AA.

AC AAB59419;

DT 22-MAR-2001 (first entry)

XX Human Class I HLA-B alpha1-domain-derived peptide #18.

KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;

KM cytotoxic T cell activation inhibition; cell transplantation;

XX natural killer cell activation inhibition; organ transplantation.

OS Homo sapiens.

PN US6162434-A.

PD 19-DEC-2000.

PF 03-MAY-1995; 95US-0433613.

PR 03-MAY-1995; 95US-0433613.

PA (SANG-) SANGSTAT MEDICAL CORP.

PI Buelow R;

DR WPI; 2001-111720/12.

XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer

PT cells involves combining cells with compound comprising oligopeptide

XX with contiguous sequence of human leukocyte antigen-B alpha1 domain

PS Disclosure; Column 7-8; 20pp; English.

XX The present sequence is a peptide which may be used in a method for

CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer

CC cells. The method involves combining the cells with a compound

CC comprising an oligopeptide of at least 6 amino acids comprising a

CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain

CC including amino acids 84-86, where amino acids 84-86 are YW.

CC The method is useful for transplanting a donor mammalian organ or cells

CC to a mammalian recipient. The organ or cells are combined with the

CC compound prior to implanting in the mammalian recipient, or the compound

CC may be administered to the mammalian recipient in a period extending

XX from prior to implanting the donor organ or cells.

XX Sequence 14 AA;

QY 4 LRIXLXYW 12
 |||||
 DB 5 LRIALRYW 13

RESULT 7
 AAG74879
 ID AAG74879 standard; Protein; 83 AA.

AC AAG74879;
 XX 03-SEP-2001 (first entry)

DT Human colon cancer antigen protein SEQ ID NO:5643.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW colorectal carcinoma.

XX Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US26524.

PR 29-SEP-1999; 99US-0157137.

PR 03-NOV-1999; 99US-0163280.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI; 2001-235357/24.

DR N-PSDB; AAH34284.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

XX useful for preventing, diagnosing and/or treating colorectal cancers -

XX Claim 11; Page 7193-7194; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon

CC cancer-associated nucleic acid molecules (N) and proteins (P), where

CC the proteins are collectively known as colon cancer antigens. The colon

CC cancer antigens have cytostatic activity and can be used in gene

CC therapy and vaccine production. N and P may be used in the prevention,

CC diagnosis and treatment of diseases associated with inappropriate P

CC expression. For example, N and P may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions

CC in a patient's genome that affect the activity of P by expressing P.

CC Additionally, N may be used to produce the colon cancer-associated Ps,

CC by inserting the nucleic acids into a host cell and culturing the cell

CC to express the proteins. N and P can be used in the prevention, diagnosis

CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204

CC and AAB77789 represent sequences used in the exemplification of the

CC present invention. 682 and page 7053 of the sequence listing were

CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were

CC missing at time of publication, meaning no sequences are present for

XX SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 83 AA;

QY 4 LRIXLXYW 12
 |||||
 DB 65 LRIALRYW 73

RESULT 8
 AAB59419
 ID AAB59419 standard; Peptide; 13 AA.

AC AAB59419;

DT 22-MAR-2001 (first entry)

XX Human Class I HLA-B alpha1-domain-derived peptide #19.

KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US6162434-A.
 XX
 PD 19-DEC-2000.
 XX
 PF 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 P1 Buelow R;
 XX
 DR WPI; 2001-111720/12.
 XX
 PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha domain -
 XX
 PS Disclosure; Column 7-8; 20pp; English.
 XX
 CC The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha domain
 CC including amino acids 84-86, where amino acids 84-86 are YYW.
 CC The method is useful for transplanting a donor mammalian organ or cells
 CC to a mammalian recipient. The organ or cells are combined with the
 CC compound prior to implanting in the mammalian recipient, or the compound
 CC may be administered to the mammalian recipient in a period extending
 CC from prior to implanting the donor organ or cells.
 XX
 SQ Sequence 13 AA;
 Query Match 62.5%; Score 35; DB 22; Length 13;
 Best Local Similarity 66.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 IXLXYYWXS 14
 Db 5 IALRYWDS 13
 DB
 RESULT 9
 ABB39053
 ID ABB39053 standard; Peptide; 37 AA.
 AC ABB39053;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #6559 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 FN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 XX
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX
 PS Claim 27; SEQ ID NO 3168; 639bp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 37 AA;
 Query Match 62.5%; Score 35; DB 22; Length 37;
 Best Local Similarity 42.9%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RXXLRXLXYYWXS 14
 Db 16 RPLRVKHFYWT 29
 DB
 RESULT 10
 AAM59705
 ID AAM59705 standard; Protein; 37 AA.
 AC AAM59705;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31810.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00667.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX

PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 31810; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 37 AA;

Query Match 62.5%; Score 35; DB 22; Length 37;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXLRIRIXLYWXS 14
Db 16 RLPLRVKHFYMTS 29

RESULT 11
AAM72285
ID AAM72285 standard; Protein; 37 AA.
XX
AC AAM72285;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32591.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 32591; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 37 AA;

Query Match 62.5%; Score 35; DB 22; Length 37;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXLRIRIXLYWXS 14
Db 16 RLPLRVKHFYMTS 29

RESULT 12
AAM32544
ID AAM32544 standard; Protein; 37 AA.
XX
AC AAM32544;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #6581 encoded by probe for measuring placental gene expression.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 27; SEQ ID NO 32813; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP;
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 37 AA;

Query Match 62.5%; Score 35; DB 22; Length 37;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXLRIRIXLYWXS 14
Db 16 RLPLRVKHFYMTS 29

RESULT 13
ABG42100
ID ABG42100 standard; Peptide; 37 AA.
XX
AC ABG42100;
XX

19-AUG-2002 (first entry)
Human peptide encoded by genome-derived single exon probe SEQ ID 31765.
Human; single exon probe; asthma; lung cancer; COPD, ILD;
Chronic obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
pulmonary histiocytosis; lymphangioleiomyomatosis; Kargener syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
primary ciliary dyskinesia; pulmonary hypertension;
hyaline membrane disease.
Homo sapiens.
WO200186003-A2.
15-NOV-2001.
30-JAN-2001; 2001WO-US00665.
04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263.
(MOLE-) MOLECULAR DYNAMICS INC.
Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2002-114183/15.
Spatially-addressable set of single exon nucleic acid probes, used to
measure gene expression in human lung samples -
Claim 27; SEQ ID No 31765; 634pp; English.
The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human lung comprising single exon nucleic acid probes having one of
12614 nucleic acid sequences mentioned in the specification, or their
complements or the 12387 open reading frames derived from the 12614
probes. Also included are a microarray comprising the novel set of
probes; the novel set of probes which hybridize at high stringency to a
nucleic acid expressed in the human lung; measuring gene expression in a
sample derived from human lung, comprising (a) contacting the array with
a collection of detectably labeled nucleic acids derived from human lung
mRNA, and (b) measuring the label detectably bound to each probe of
the array; identifying exons in a eukaryotic genome, comprising
(a) algorithmically predicting at least one exon from genomic sequences
of the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
in the above mentioned microarray; assigning sequence to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene
expression analysis, and for identifying exons in a gene, particularly
using human lung derived mRNA and for the study of lung diseases
such as asthma, lung cancer, chronic obstructive pulmonary disease
(COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
fibrosis, neurofibromatosis, tuberosus sclerosis, Gaucher's disease,
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,

pulmonary alveolar proteinosis, Kargener syndrome, fibrocystic
pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
and hyaline membrane disease. The present sequence is a peptide/protein
encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp://wipo.int/pub/published_pct_sequences.
SQ Sequence 37 AA:
Query Match 62.5%; Score 35; DB 23; Length 37;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RXXLRRLXLYYKXS 14
DB 16 RLPLRVKHFYWTSS 29
RESULT 14
AAW17668
ID AAW17668 standard; peptide; 68 AA.
AC AAW17668;
XX
XX
DT 16-DEC-1997 (first entry)
XX
XX
DE Stem cell mobilising chemokine CXbeta-13.
XX
XX
KW Haematopoietic cell; parasitic infection; colony stimulating factor;
KW haematopoietic cell; immune response; bacterial infection; transplant;
KW wound healing; bone marrow; immunosuppression; regeneration;
KW neoplastic disease; viral disease; gene therapy; cytotoxic drug.
XX
OS Synthetic.
XX
XX
PN WO9715594-A1.
XX
XX
PD 01-MAY-1997.
XX
XX
PF 23-OCT-1996; 96WO-US16959.
XX
XX
PR 24-OCT-1995; 95US-0006051.
XX
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX
PI Kreider BL, Li H, Pelus L, White JR;
XX
XX
DR WPI; 1997-258956/23.
XX
XX
PT Ten new chemokine(s) able to mobilise stem cells - used where
PT increased levels of haematopoietic cells are required, e.g. to
PT increase resistance to infection
XX
XX
PS Claim 10; Page 13; 24pp; English.
XX
XX
CC The present sequence represents a chemokine, CXbeta-13, which is capable
CC of mobilising stem cells. The chemokine can be used therapeutically to
CC improve stem cell mobilisation, optionally together with a colony
CC stimulating factor or other haematopoietic agent. It can be used
CC wherever an increased level of haematopoietic cells is needed, e.g. to
CC increase the immune response to chronic infection (particularly
CC bacterial or parasitic), to promote wound healing, in (transplant)
CC patients with reduced bone marrow function as a result of
CC immunosuppressive treatment or disease, and to provide more rapid
CC regeneration of bone marrow after treatment for neoplastic or viral
CC diseases. The induced stem cells may be harvested for subsequent return
CC to the patient, optionally after they have been genetically manipulated
CC to deliver a selected gene product (gene therapy). The cells may be
CC co-administered with a cytotoxic drug.
XX
SQ Sequence 68 AA;

Query Match 62.5%; Score 35; DB 18; Length 68;
 Best Local Similarity 42.9%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RXLRRLXLYYXKS 14
 | | | | |
 DB 19 RLPLRVVGHFYWTS 32

RESULT 15

AAW20061
 ID AAW20061 standard; Protein: 69 AA.

AC AAW20061;

DT 11-SEP-1997 (first entry)

DE Human macrophage derived chemokine analogue.

KW MDC, macrophage derived chemokine; C-C; Cys-Cys; Crohn's disease;
 rheumatoid arthritis; chemotaxis; fibroblast proliferation;
 wound healing; angiogenesis; inflammation.

OS Synthetic.

PN W09640923-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-US10114.

PR 16-NOV-1995; 95US-0558658.

PR 07-JUN-1995; 95US-0479620.

PA (ICOS-) ICOS CORP.

PI Godiska R, Gray PW;

DR WPI; 1997-052324/05.

PT Macrophage derived chemokine (MDC) and analogues - used in the
 treatment of inflammatory diseases, MDC antibodies used to treat
 Crohn's disease, rheumatoid arthritis, etc.

PS Claim 25; Page 84; 106pp; English.

CC A new macrophage derived chemokine, MDC, a member of the C-C
 (Cys-Cys) subfamily of cytokines has been isolated. MDC and its
 analogues may be used in the treatment of inflammatory diseases
 especially diseases characterised by monocyte chemotaxis towards a
 site of inflammation. MDC and its analogues also induce fibroblast
 proliferation having a positive effect in wound healing and
 angiogenesis. They may prove to be clinically important in the
 treatment of tumours, by directly or indirectly inhibiting tumour
 formation. Antibodies directed against MDC and its analogues may be
 used in the treatment of Crohn's disease, rheumatoid arthritis and
 atherosclerosis. Probes and/or primers for the identification of MDC
 encoding sequences can be derived from MDC encoding sequences.

SO Sequence 69 AA;

Query Match 62.5%; Score 35; DB 18; Length 69;

Best Local Similarity 42.9%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RXLRRLXLYYXKS 14
 | | | | |
 DB 20 RLPLRVVGHFYWTS 33

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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:02:45 ; Search time 17 Seconds
(without alignments)
71.060 Million cell updates/sec

Title: US-09-742-148A-3
Perfect score: 56
Sequence: 1 RXXLRILXLYYXMS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues
Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.dep.*
2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.dep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.dep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.dep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.dep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.dep.*
7: /cgn2_6/ptodata/2/pubpaa/PTCT_PUBCOMB.dep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.dep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.dep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.dep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.dep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.dep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.dep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	62.5	37	10	US-09-864-761-43730
2	35	62.5	93	9	US-09-811-088-2
3	35	62.5	93	10	US-09-837-446-6
4	35	62.5	93	10	US-09-908-599-2
5	35	62.5	93	10	US-09-908-600-2
6	33	58.9	79	10	US-09-864-761-47994
7	33	58.9	184	9	US-09-858-580-21
8	33	58.9	184	9	US-09-847-172-21
9	31	55.4	120	9	US-09-738-626-6631
10	31	55.4	256	10	US-09-815-242-10664
11	31	55.4	272	9	US-09-712-363-276
12	31	55.4	272	9	US-09-813-453A-5
13	31	55.4	365	9	US-10-101-464A-901
14	31	55.4	446	9	US-10-101-464A-733
15	31	55.4	3084	10	US-09-938-275-4
16	30	53.6	176	9	US-10-101-464A-748
17	30	53.6	186	9	US-09-862-810-8
18	29	51.8	18	10	US-09-103-067-16
19	29	51.8	22	10	US-09-103-067-5

20	29	51.8	52	9	US-10-185-050-120	Sequence 120, App
21	29	51.8	62	10	US-09-864-761-47836	Sequence 47836, A
22	29	51.8	70	9	US-10-101-464A-524	Sequence 524, App
23	29	51.8	87	9	US-10-091-438-129	Sequence 129, App
24	29	51.8	122	9	US-10-102-806-613	Sequence 613, App
25	29	51.8	144	9	US-10-102-806-773	Sequence 773, App
26	29	51.8	151	10	US-09-789-561-170	Sequence 170, App
27	29	51.8	170	10	US-09-811-284-206	Sequence 206, App
28	29	51.8	219	10	US-09-355-000-2	Sequence 2, Appli
29	29	51.8	219	10	US-09-355-000-3	Sequence 3, Appli
30	29	51.8	219	10	US-09-355-000-4	Sequence 4, Appli
31	29	51.8	219	10	US-09-355-000-5	Sequence 5, Appli
32	29	51.8	219	10	US-09-355-000-6	Sequence 6, Appli
33	29	51.8	219	10	US-09-355-000-7	Sequence 7, Appli
34	29	51.8	219	10	US-09-355-000-8	Sequence 8, Appli
35	29	51.8	219	10	US-09-355-000-9	Sequence 9, Appli
36	29	51.8	219	10	US-09-355-000-10	Sequence 10, Appli
37	29	51.8	263	10	US-09-355-000-11	Sequence 11, Appli
38	29	51.8	295	10	US-09-103-067-20	Sequence 20, Appli
39	29	51.8	295	10	US-09-949-192-3	Sequence 3, Appli
40	29	51.8	318	9	US-09-738-626-4955	Sequence 4955, Ap
41	29	51.8	420	10	US-09-741-669-425	Sequence 425, App
42	29	51.8	502	10	US-09-779-429-1	Sequence 1, Appli
43	29	51.8	591	10	US-09-867-586A-24	Sequence 24, Appli
44	29	51.8	591	10	US-09-903-012-24	Sequence 24, Appli
45	29	51.8	2799	9	US-10-151-726-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-864-761-43730
Sequence 43730, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43730
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004382.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
OTHER INFORMATION: EST HUMAN HIT: W61230.1, EVALU8 8.50e-01
US-09-864-761-43730

Query Match 62.5%; Score 35; DB 10; Length 37;
Best Local Similarity 42.9%; Pred. No. 5.9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXXLRIXLXYWXS 14
Db 16 RLPLRVKHFYWTS 29

RESULT 2
US-09-811-088-2
Sequence 2, Application US/09811088
Patent No. US20020160446A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Geating, David P.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER
FILE REFERENCE: 07334-324001
CURRENT APPLICATION NUMBER: US/09/811,088
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 09/712,726
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 08/820,364
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 09/757,421
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 08/843,652
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: US 08/843,651
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: US 09/354,809
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/938,365
PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FaestSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
US-09-811-088-2

Query Match 62.5%; Score 35; DB 9; Length 93;
Best Local Similarity 42.9%; Pred. No. 14;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 RXXLRIXLXYWXS 14
Db 44 RLPLRVKHFYWTS 57

RESULT 3
US-09-837-446-6
Sequence 6, Application US/09837446
Patent No. US20020019341A1
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Campbell, James J.
APPLICANT: Rottman, James B.
APPLICANT: Wu, Lijian
TITLE OF INVENTION: Modulation of Systemic Memory T Cell
FILE REFERENCE: STAN-110CON
CURRENT APPLICATION NUMBER: US/09/837,446
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/232,878
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FaestSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 93
TYPE: PRT
ORGANISM: H. sapiens
US-09-837-446-6

Query Match 62.5%; Score 35; DB 10; Length 93;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXXLRIXLXYWXS 14
Db 44 RLPLRVKHFYWTS 57

RESULT 4
US-09-908-599-2
Sequence 2, Application US/09908599
Patent No. US20020055147A1
GENERAL INFORMATION:
APPLICANT: Li, Haodong et al.
TITLE OF INVENTION: Human Chemokine Beta 13
FILE REFERENCE: PFI77P3
CURRENT APPLICATION NUMBER: US/09/908,599
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/432,768
PRIOR FILING DATE: 1999-11-03
PRIOR APPLICATION NUMBER: 60/032,432
PRIOR FILING DATE: 1996-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
US-09-908-599-2

Query Match 62.5%; Score 35; DB 10; Length 93;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXXLRIXLXYWXS 14
Db 44 RLPLRVKHFYWTS 57

RESULT 5
US-09-908-600-2

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PRIORITY APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47994
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AB023057.1
OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 0.67
OTHER INFORMATION: EST HUMAN HIT: BE896125.1, EVALU8 1.00e-36
OTHER INFORMATION: SWISSPROT HIT: P01893, EVALU8 8.00e-42
US-09-864-761-47994

Query Match 58.9%; Score 33; DB 10; Length 79;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

CY 1 EXXIRIXLYY 11
      |||||
Db 64 RENDRLALRY 74

RESULT 7
US-09-858-580-21
Sequence 21, Application US/09858580
Patent No. US20020176864A1
GENERAL INFORMATION:
APPLICANT: Burrows et al.
TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of
FILE REFERENCE: 48823
CURRENT APPLICATION NUMBER: US/09/858,580
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/064,552
PRIOR FILING DATE: 1997-09-16
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21

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/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-858-580-21

Query Match 58.9%; Score 33; DB 9; Length 184;
Best Local Similarity 63.6%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLY 11
DB 75 RENTRLRLRY 85

RESULT 8
US-09-847-172-21
/ Sequence 21, Application US/09847172
/ Publication No. US2003007978A1
/ GENERAL INFORMATION:
/ APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY
/ APPLICANT: BURROWS, GREGORY G.
/ APPLICANT: VANDENBARK, ARTHUR A.
/ TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPEC
/ TITLE OF INVENTION: CELLS
/ FILE REFERENCE: 899-58137
/ CURRENT APPLICATION NUMBER: US/09/847,172
/ CURRENT FILING DATE: 2001-05-01
/ PRIOR APPLICATION NUMBER: US 60/200,942
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 09/153,586
/ PRIOR FILING DATE: 1998-09-15
/ PRIOR APPLICATION NUMBER: US 60/064,555
/ PRIOR FILING DATE: 1997-10-10
/ PRIOR APPLICATION NUMBER: US 60/064,552
/ PRIOR FILING DATE: 1997-09-16
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 21
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-847-172-21

Query Match 58.9%; Score 33; DB 9; Length 184;
Best Local Similarity 63.6%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLY 11
DB 75 RENTRLRLRY 85

RESULT 9
US-09-738-626-6631
/ Sequence 6631, Application US/09738626
/ Publication No. US20020197605A1
/ GENERAL INFORMATION:
/ APPLICANT: NAKAGAWA, SATOSHI
/ APPLICANT: MIZOGUCHI, HIROSHI
/ APPLICANT: ANDO, SEIKO
/ APPLICANT: HAYASHI, MIKIRO
/ APPLICANT: OCHIAI, KEIKO
/ APPLICANT: YOKOI, HARUHIKO
/ APPLICANT: TATEISHI, NAOKO
/ APPLICANT: SENO, AKIHIRO
/ APPLICANT: IKEDA, MASATO
/ APPLICANT: OZAKI, AKIO
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-125
/ CURRENT APPLICATION NUMBER: US/09/738,626
/ CURRENT FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: JP 99/377484
/ PRIOR FILING DATE: 1999-12-16

/ PRIOR APPLICATION NUMBER: JP 00/159162
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: JP 00/280988
/ PRIOR FILING DATE: 2000-08-03
/ NUMBER OF SEQ ID NOS: 7059
/ SOFTWARE: Patent in ver. 3.0
/ SEQ ID NO 6631
/ LENGTH: 120
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-6631

Query Match 55.4%; Score 31; DB 9; Length 120;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 LRLXLYY 12
DB 42 LRLVLYY 50

RESULT 10
US-09-815-242-10664
/ Sequence 10664, Application US/09815242
/ Patent No. US2002061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10664
/ LENGTH: 256
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-09-815-242-10664

Query Match 55.4%; Score 31; DB 10; Length 256;
Best Local Similarity 71.4%; Pred. No. 1,8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IXLXLYY 12
DB 93 IGLDYLYY 99

RESULT 11
US-09-712-363-276
/ Sequence 276, Application US/09712363

Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
FILE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 276
LENGTH: 272
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-276

Query Match 55.4%; Score 31; DB 9; Length 272;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRXLXYYWXS 14
DB 74 VRIMLDQYWPS 84

RESULT 12
US-09-813-453A-5
Sequence 5, Application US/09813453A
Patent No. US20020168681A1
GENERAL INFORMATION:
APPLICANT: Vocum, R. Rogers
APPLICANT: Patterson, Thomas A.
TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
FILE OF INVENTION: ANTIBIOTICS
FILE REFERENCE: CG2-001
CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/227,860
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/667,569
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 272
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-813-453A-5

Query Match 55.4%; Score 31; DB 9; Length 272;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRXLXYYWXS 14
DB 74 VRIMLDQYWPS 84

RESULT 13
US-10-101-464A-901
Sequence 901, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 901
LENGTH: 365
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-901

Query Match 55.4%; Score 31; DB 9; Length 365;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IXLXYYW 12
DB 277 IFLVYIW 283

RESULT 14
US-10-101-464A-733
Sequence 733, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 733
LENGTH: 446
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-733

Query Match 55.4%; Score 31; DB 9; Length 446;

Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 IXLXYW 12
DB 277 IFLVYW 283

RESULT 15
US-09-938-275-4
; Sequence 4; Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3084
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P19137
; DATABASE ENTRY DATE: 1990-11-01
US-09-938-275-4

Query Match 55.4%; Score 31; DB 10; Length 3084;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 RIXLYYWX 14
DB 569 RLSTYYMA 578

Search completed: May 5, 2003, 14:11:10
Job time : 19 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:00:15 ; Search time 29 Seconds
(without alignments)
14.204 Million cell updates/sec

Title: US-09-742-148a-3

Sequence: 1 RXXLRILXYYWXS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	82.1	14	1	US-08-440-504A-3
2	46	82.1	14	4	US-08-433-613-3
3	41	73.2	10	4	US-08-433-613-57
4	41	73.2	14	4	US-08-433-613-17
5	41	73.2	14	4	US-08-433-613-18
6	35	62.5	13	4	US-08-433-613-19
7	35	62.5	69	2	US-08-660-542-31
8	35	62.5	70	2	US-08-660-542-30
9	35	62.5	93	1	US-08-480-449-2
10	35	62.5	93	2	US-08-660-542-2
11	35	62.5	93	4	US-09-232-878-6
12	35	62.5	93	4	US-08-479-603-2
13	35	62.5	93	5	PCT-US95-07294-2
14	34	60.7	182	1	US-08-127-954-154
15	34	60.7	182	1	US-08-127-954-162
16	33	58.9	182	1	US-08-127-954-150
17	33	58.9	182	1	US-08-127-954-151
18	33	58.9	182	1	US-08-127-954-152
19	33	58.9	182	1	US-08-127-954-153
20	33	58.9	184	4	US-09-153-586-21
21	31	55.4	13	4	US-08-433-613-20
22	31	55.4	13	4	US-08-433-613-21
23	30	53.6	14	4	US-08-433-613-16
24	30	53.6	525	4	US-09-273-163-5
25	30	53.6	627	4	US-09-273-163-4
26	30	53.6	660	4	US-09-273-163-6
27	27	53.6	2233	2	US-08-569-853-1

28	30	53.6	2233	2	US-08-569-853-2	Sequence 2, Appli
29	30	53.6	2233	3	US-08-987-439-1	Sequence 1, Appli
30	29	51.8	22	1	US-07-924-030-2	Sequence 2, Appli
31	29	51.8	22	2	US-08-372-887-5	Sequence 5, Appli
32	29	51.8	52	2	US-08-630-916A-120	Sequence 120, App
33	29	51.8	118	2	US-08-652-816A-13	Sequence 13, Appli
34	29	51.8	218	1	US-07-816-679A-3	Sequence 3, Appli
35	29	51.8	218	5	PCT-US92-11270-3	Sequence 3, Appli
36	29	51.8	219	2	US-08-479-733A-23	Sequence 23, Appli
37	29	51.8	219	3	US-08-487-437-23	Sequence 23, Appli
38	29	51.8	219	3	US-08-479-727A-23	Sequence 23, Appli
39	29	51.8	219	3	US-08-482-369A-23	Sequence 23, Appli
40	29	51.8	219	4	US-09-009-217-9	Sequence 9, Appli
41	29	51.8	219	4	US-09-009-656-9	Sequence 9, Appli
42	29	51.8	219	5	PCT-US95-07439-23	Sequence 23, Appli
43	29	51.8	220	4	US-09-009-217-1	Sequence 1, Appli
44	29	51.8	220	4	US-09-009-217-4	Sequence 4, Appli
45	29	51.8	220	4	US-09-009-217-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-440-504A-3
; Sequence 3, Application US/08440504A
; Patent No. 5753625
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Treatment for Inhibiting the Progression
; OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Flehr, Hohbach, Teet, Albitron & Herbert
; STREET: 4 Embarradero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,504A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccarlin, Richard F.
; REGISTRATION NUMBER: 31,801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO.: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "The 'X' at position can
; OTHER INFORMATION: either be Valine or Glutamic Acid."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "The 'X' at position three
; OTHER INFORMATION: can either be Asparagine or Aspartic Acid."
; FEATURE:

NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "The 'X' at position 7 can
OTHER INFORMATION: either be Alanine or Leucine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "The 'X' at position 9 can
OTHER INFORMATION: either be Arginine or Glutamic Acid."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note= "The 'X' at position 13 can
OTHER INFORMATION: either be Glutamine or Aspartic Acid."
US-08-440-504A-3

Query Match 82.1%; Score 46; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXLRIXLYYMXS 14
DB 1 RXXLRIXLYYMXS 14

RESULT 2
US-08-433-613-3
Sequence 3, Application US/08433613A

PATENT NO. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (2)
OTHER INFORMATION: The amino acid at position 2 can be either Valine
OTHER INFORMATION: or Glutamic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (3)
OTHER INFORMATION: The amino acid at position 3 can be either
OTHER INFORMATION: Asparagine or Aspartic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
OTHER INFORMATION: The amino acid at position 7 can be either Alanine
OTHER INFORMATION: or Leucine.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (9)
OTHER INFORMATION: The amino acid at position 9 can be either
OTHER INFORMATION: Arginine or Glutamic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (13)
OTHER INFORMATION: The amino acid at position 13 can be either
OTHER INFORMATION: Glutamine or Aspartic acid.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-3

Query Match 82.1%; Score 46; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXXLRIXLYYMXS 14
DB 1 RXXLRIXLYYMXS 14

RESULT 3
US-08-433-613-57
Sequence 57, Application US/08433613A

PATENT NO. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-57

Query Match 73.2%; Score 41; DB 4; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.085;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIXLYY 12
DB 2 LRIALRYW 10

RESULT 4
US-08-433-613-17

Sequence 17, Application US/08433613A
PATENT NO. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-17

Query Match 73.2%; Score 41; DB 4; Length 14;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIXLYY 12
DB 6 LRIALRYW 14

RESULT 5
US-08-433-613-18

Sequence 18, Application US/08433613A
PATENT NO. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland

```

; TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
; OPERATING SYSTEM: PC-DOS/MS-DOS
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-18

Query Match
Best Local Similarity 73.2%; Score 41; DB 4; Length 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LRLXLYYW 12
Db 5 LRLXLYYW 13

RESULT 6
US-08-433-613-19
; Sequence 19, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-19

Query Match
Best Local Similarity 62.5%; Score 35; DB 4; Length 13;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 IXLXYWXS 14
Db 5 IALRYWDS 13

RESULT 7
US-08-660-542-31
; Sequence 31, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/33318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-542-31

Query Match
Best Local Similarity 42.9%; Score 35; DB 2; Length 69;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RXXLRXLYWXS 14
Db 20 RPLRVKHFYWT 33

RESULT 8
US-08-660-542-30
; Sequence 30, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
```

REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/33318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-542-30

Query Match 62.5%; Score 35; DB 2; Length 70;
Best Local Similarity 42.9%; Pred. No. 6.8;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXLRRLXLYWXS 14
DB 21 RLPLRVVXHFYWT 34

RESULT 9
US-08-480-449-2
Sequence 2, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-449-2

Query Match 62.5%; Score 35; DB 1; Length 93;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXLRRLXLYWXS 14
DB 44 RLPLRVVXHFYWT 57

RESULT 10
US-08-660-542-2
Sequence 2, Application US/08660542
Patent No. 5932703
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-542-2

Query Match 62.5%; Score 35; DB 2; Length 93;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXLRRLXLYWXS 14
DB 44 RLPLRVVXHFYWT 57

RESULT 11
US-09-232-878-6
Sequence 6, Application US/09232878
Patent No. 6245332
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene
APPLICANT: Campbell, James
APPLICANT: Rottman, James
TITLE OF INVENTION: Modulation of Systemic Memory T cell Trafficking
FILE REFERENCE: SUN-110PRV
CURRENT APPLICATION NUMBER: US/09/232,878
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6
LENGTH: 93
TYPE: PRT
ORGANISM: H. sapiens
US-09-232-878-6

Query Match 62.5%; Score 35; DB 4; Length 93;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXXLRXIXYYWXS 14
DB 44 RLPRLRVKHFYMTS 57

RESULT 12
US-08-479-603-2
Sequence 2, Application US/08479603
Patent No. 6320023

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6100 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,603
FILING DATE:

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32780
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-603-2

Query Match 62.5%; Score 35; DB 4; Length 93;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXXLRXIXYYWXS 14
DB 44 RLPRLRVKHFYMTS 57

RESULT 13
PCT-US95-07294-2
Sequence 2, Application PC/US9507294
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Chemokine Beta-13
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSER: CARELLA, BYRNE, BAIN, GILFILLIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07294
FILING DATE: June 6, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/464,594
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-356
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-07294-2

Query Match 62.5%; Score 35; DB 5; Length 93;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RXXLRXIXYYWXS 14
DB 44 RLPRLRVKHFYMTS 57

RESULT 14
US-08-127-954-154
Sequence 154, Application US/08127954
Patent No. 5451512

GENERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Teodorica L.
TITLE OF INVENTION: Methods and Reagents for HLA Class I A
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
FILING DATE:

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.

Search completed: May 5, 2003, 14:03:38
Job time : 30 secs

REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-127-954-154

Query Match 60.7%; Score 34; DB 1; Length 182;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLY 11
DB 75 RESLRRLRY 85

RESULT 15

US-08-127-954-162
Sequence 162, Application US/08127954
Patent No. 5451512
GENERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Teodorica L.
TITLE OF INVENTION: Methods and Reagents for HLA Class I A
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-127-954-162

Query Match 60.7%; Score 34; DB 1; Length 182;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRRLXLY 11
DB 75 RESLRRLRY 85

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:10:51 ; Search time 43 Seconds
(without alignments)
31.300 Million cell updates/sec

Title: US-09-742-148A-3

Perfect score: 56
Sequence: 1 RXLRRLXLYWXS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2093

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	44.6	12	2	PH1324
2	24	42.9	12	2	I57678
3	20	35.7	10	2	PT0291
4	20	35.7	12	2	G64003
5	20	35.7	14	2	S03530
6	20	35.7	14	2	PH1608
7	19	33.9	12	2	S25056
8	19	33.9	13	2	PH1596
9	19	33.9	14	2	PT0232
10	19	33.9	14	2	PT0252
11	18	32.1	9	2	PT0324
12	18	32.1	10	2	S71868
13	18	32.1	10	2	F33932
14	18	32.1	11	2	S32575
15	18	32.1	11	2	PH1308
16	18	32.1	12	2	PN0046
17	18	32.1	13	2	A05174
18	18	32.1	13	2	A61514
19	18	32.1	13	2	B28610
20	18	32.1	13	2	S32551
21	18	32.1	14	2	PT0223
22	18	32.1	14	2	PH1348
23	18	32.1	14	2	PH1322
24	18	32.1	14	2	S39931
25	17	30.4	8	2	S68325
26	17	30.4	11	2	S19775
27	17	30.4	12	2	S18722
28	17	30.4	14	2	C60414
29	17	30.4	14	2	B60842

30	17	30.4	14	2	A60622	somatostatin - spo
31	17	30.4	14	2	A60840	somatostatin I - E
32	17	30.4	14	2	S00172	somatostatin I - s
33	17	30.4	14	2	JH0328	probrusin tetrade
34	17	30.4	14	2	A35105	hypothetical prote
35	16	28.6	8	2	US0318	leucokinin VIII -
36	16	28.6	9	2	PT0272	Ig heavy chain CRD
37	16	28.6	9	2	PT0285	Ig heavy chain CRD
38	16	28.6	10	2	PT0245	Ig heavy chain CRD
39	16	28.6	14	2	PH1639	Ig H chain V-D-J r
40	16	28.6	14	2	PH1597	Ig H chain V-D-J r
41	16	28.6	14	2	PH1601	Ig H chain V-D-J r
42	15	26.8	10	2	C39191	hypothetical prote
43	15	26.8	10	2	A2114	gonadolibetin - ch
44	15	26.8	10	2	C41946	T-cell receptor ga
45	15	26.8	12	2	PT0274	Ig heavy chain CRD

ALIGNMENTS

RESULT 1
PH1324
Ig heavy chain DJ region (clone C510-100) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1324
R:Maeserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A>Title: Predominance of fetal type DH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1324
A:Molecule type: DNA
A:Residues: 1-12 <WAS>
C:Keywords: heterotrimer; immunoglobulin

Query Match 44.6%; Score 25; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YYW 12
DB 6 YYW 8

RESULT 2
I57678
gene rPLP-A protein - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C:Accession: I57678
R:Vuille, U.C.; Calcini, P.A.; Bock, M.E.; Verstyuf, A.; Schroeder, I.C.; Duckworth, M.
Mol. Cell. Endocrinol. 96, 91-98, 1993
A>Title: Rat prolactin-like protein A partial gene and promoter structure: promoter acti
A:Reference number: I57678; MUID:94102438; PMID:8276144
A:Accession: I57678
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:S68117; NID:G544690
C:Genetics:

Query Match 42.9%; Score 24; DB 2; Length 12;
Best Local Similarity 27.3%; Pred. No. 1.5e+02;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 LRRLXLYWXS 14
DB 1 WHLSLHWS 11

RESULT 3

PT0291
Ig heavy chain CRD3 region (clone 4-115B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0291
R:Yamada, M.; Masseman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0291
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.7%; Score 20; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 IXLYYXWS 14
| | | | |
Db 2 ISPTYYYS 10

RESULT 4
G64003
hypothetical protein HI0195 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C:Accession: G64003
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kikness, E.F.; Kerlavage, A.
J. Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Author: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
C:Accession: G64003
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <TIGR>
A:Cross-references: GB:U02704; GB:I42023; NID:g1573153; PID:g1573155; TIGR:HI0195

Query Match 35.7%; Score 20; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 YVW 12
| | |
Db 6 HW 8

RESULT 5
S03530
Ig heavy chain J region (JH-4) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
C:Accession: S03530
R:Schwager, J.; Grosberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus
A:Reference number: S01158; MUID:89052653; PMID:2903824
C:Accession: S03530
A:Molecule type: DNA
A:Residues: 1-14 <SCH>
A:Cross-references: EMBL:X14918; NID:g64805; PID:CAA33043.1; PID:g1334657

Query Match 35.7%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 YVW 12
| | |

Db 2 YHW 4

RESULT 6
PH1608
Ig H chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1608; PH1603
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
C:Accession: PH1608
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 335
A:Accession: PH1603
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 324
C:Keywords: immunoglobulin

Query Match 35.7%; Score 20; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 RIXLYYV 12
| | | | |
Db 3 RVGNSTYY 10

RESULT 7
S25056
Ig heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25056
R:Jacob, J.; Kelsce, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A:Reference number: S25024
C:Accession: S25056
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <JAC>
A:Cross-references: EMBL:X67386; NID:g50927; PID:CAA47798.1; PID:g1333920
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YVXWS 14
| | | | |
Db 5 YVXWS 9

RESULT 8
PH1596
Ig H chain V-D-J region (wild-type clone 303) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1596
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
C:Accession: PH1596
A:Molecule type: DNA
A:Residues: 1-13 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match

33.9%; Score 19; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 LXYW 12

DB 5 LGYY 9

RESULT 9

PT0232

Ig heavy chain CRD3 region (clone 1-124) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0232

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0232

A:Molecule type: DNA

A:Residues: 1-14 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

33.9%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 YXWXS 14

DB 3 YYYS 7

RESULT 10

PT0252

Ig heavy chain CRD3 region (clone 2-109D) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0252

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0252

A:Molecule type: DNA

A:Residues: 1-14 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

33.9%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 YXWXS 14

DB 4 YYYS 8

RESULT 11

PT0324

Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0324

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Residues: 1-9 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12

DB 8 YW 9

RESULT 12

S71868

glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)

M:Alternate names: glutathione S-transferase class mu 4

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 07-May-1999

C:Accession: S71868

R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospira

A:Reference number: S71864; MUID:96332484; PMID:8760377

A:Accession: S71868

A:Molecule type: protein

A:Residues: 1-10 <ROU>

C:Comment: At least five species-independent classes of cytosolic glutathion transferase

S mitochondrial form are known.

C:Complex: dimer

C:Function:

A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a

A:Pathway: detoxification; xenobiotics metabolism

A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

es of damage

C:Superfamily: glutathione transferase

C:Keywords: dimer; transferase

Query Match

32.1%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12

DB 5 YW 6

RESULT 13

F33932

Ig mu chain J region (E7) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996

C:Accession: F33932

R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A:Title: Two murine natural polyclonal antibodies are encoded by nonmutated germ-1

A:Reference number: A33932; MUID:89282823; PMID:2499887

A:Accession: F33932

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-10 <BAC>

A:Cross-references: GB:M27106

C:Keywords: immunoglobulin

Query Match

32.1%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12

DB 4 YW 5

RESULT 14

S32575
ribosomal protein S2, plasmid - squawroot plasmid (fragment)
C:Species: plasmid Conopholis americana (squawroot)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C:Accession: S32575
R:Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A:Title: Lack of a functional plasmid rRNA(Cys) gene is associated with loss of photosyn
A:Reference number: S32575, MUID:92145776, PMID:1723564
A:Accession: S32575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <TAY>
A:Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C:Genetics:
A:Gene: rps2
A:Genome: plasmid
C:Superfamily: Escherichia coli ribosomal protein S2
C:Keywords: plasmid; protein biosynthesis; ribosome

Query Match

Best Local Similarity 32.1%; Score 18; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
||

DB 5 YW 6

RESULT 15

PH1308
Ig heavy chain DJ region (clone C731-94) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1308
R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1308
A:Molecule type: DNA
A:Residues: 1-12 <WAS>
C:Keywords: heterodimer; immunoglobulin

Query Match

Best Local Similarity 32.1%; Score 18; DB 2; Length 12;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
||

DB 6 YW 7

Search completed: May 5, 2003, 14:14:28
Job time : 45 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:03:45 ; Search time 11 Seconds
(without alignments)
52.788 Million cell updates/sec

Title: US-09-742-148A-3
Perfect score: 56
Sequence: 1 RXXLRILXLYYXKS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 633

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.1	11	1	RR2_CONAM
2	18	32.1	13	1	TP13_PHYRO
3	17	30.4	14	1	SMS1_MYOSC
4	17	30.4	14	1	SMS1_MYOSC
5	16	28.6	8	1	LCK8_LEUMA
6	16	28.6	8	1	URPA_HUMAN
7	15	26.8	10	1	GON3_ONCKE
8	15	26.8	14	1	LPW_RHIME
9	14	25.0	9	1	DI_NEPNO
10	14	25.0	12	1	UR2A_CATCO
11	14	25.0	12	1	UR2B_CATCO
12	14	25.0	12	1	UR2B_CYPCA
13	14	25.0	12	1	UR2_GILMT
14	14	25.0	12	1	UR2_POLSP
15	14	25.0	12	1	UR2_SCYCA
16	14	25.0	13	1	TEML_RANTE
17	14	25.0	14	1	CXA1_CONCN
18	13	23.2	9	1	FARP_CALST
19	13	23.2	10	1	GON1_AULMT
20	13	23.2	10	1	GON1_CHEPR
21	13	23.2	10	1	GON1_CHEPR
22	13	23.2	10	1	GON2_CHEPR
23	13	23.2	10	1	GON2_CHEPR
24	13	23.2	10	1	GON3_PETMA
25	13	23.2	10	1	GONL_SQUAC
26	13	23.2	10	1	GRP_RANRI
27	13	23.2	11	1	LPW_THETH
28	13	23.2	11	1	NOA0_LOTUA
29	13	23.2	14	1	LPW_CITFR
30	13	23.2	14	1	LPW_ECOTI
31	13	23.2	14	1	LPW_SALTY
32	13	23.2	14	1	NEJ2_FASHE
33	12	21.4	7	1	PARI_PROCL

34	12	21.4	7	1	FAR2_PROCL
35	12	21.4	8	1	FAR3_HOMAM
36	12	21.4	8	1	FAR4_HOMAM
37	12	21.4	9	1	LITR_PHYRO
38	12	21.4	10	1	ABE_CARGI
39	12	21.4	11	1	COR2_PETAM
40	12	21.4	11	1	ESI_RAT
41	12	21.4	11	1	MIG_THETS
42	12	21.4	11	1	RANC_RANPI
43	12	21.4	13	1	MIA_ANOCA
44	12	21.4	13	1	MIA_CAMDR
45	12	21.4	14	1	LPF2_ECOTI

ALIGNMENTS

```

RESULT 1
ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN P852.
OS Comopholis americana (Squawroot).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Orobanchaceae; Comopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
RT of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X64567; CAA45868.1; -
DR InterPro; IPR001865; Ribosomal S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON TER 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536844 CRC64;

Query Match 32.1%; Score 18; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
Db 5 YW 6

RESULT 2
ID TP13_PHYRO STANDARD; PRT; 13 AA.
AC P04056;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Trypophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxId=8394;
RN (1)
RP SEQUENCE.
RA Montecuchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
tridecapeptide from Phyllomedusa rohdei".
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -1- TISSUE SPECIFICITY: SECRETED.
DR PIR; A05174; A05174.
KW Amphibian skin.
FT MOD RES
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;
Query Match 32.1%; Score 18; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 YW 12
DB 5 YW 6
RESULT 3
SMS_MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (shorthorn sculpin) (Daddy sculpin),
OS Onchorynchus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Corioidae; Coriidae; Myoxocephalus.
OX NCBI_TaxId=8097, 8019, 7936;
RN (1)
RN SEQUENCE.
RP SPECIES=M.scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RT Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
prosomatostatins I and II isolated from the pancreatic islets of two
species-of teleostean fish: the daddy sculpin and the flounder".
RL Eur. J. Biochem. 168:647-652(1987).
RN (2)
RN SEQUENCE.
RP SPECIES=O.kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Piletskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorman A.;
RT "Characterization of coho salmon (Onchorynchus kisutch) islet
somatostatins".
RL Gen. Comp. Endocrinol. 63:252-263(1986).
RN (3)
RN SEQUENCE.
RP SPECIES=A.anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
structural features from the European eel (Anguilla anguilla)".
RL Gen. Comp. Endocrinol. 72:181-189(1988).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR PIR; S00172; S00172.

DR PIR; B60842; B60842.
DR PIR; A60840; A60840.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin, 1.
KW Hormone; Multigene family.
FT DISULFID
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
Query Match 30.4%; Score 17; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 YW 12
DB 6 FFW 8
RESULT 4
SMS_ALLMT STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxId=8496, 34903;
RN (1)
RN SEQUENCE.
RP SPECIES=A.mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
and stomach of the alligator".
RL Peptides 14:573-579(1993).
RN (2)
RN SEQUENCE.
RP SPECIES=T.scripta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
somatostatin from the turtle, Pseudemys scripta".
RL Peptides 11:461-466(1990).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR PIR; C60414; C60414.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin, 1.
KW Hormone.
FT DISULFID
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
Query Match 30.4%; Score 17; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 YW 12
DB 6 FFW 8
RESULT 5
LCK8_LEUMA STANDARD; PRT; 8 AA.
AC P19930;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).

OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaea.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR, JS0318; JS0318.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 902 MW; 736365AB59CADD8 CRC64;
 AMIDATION.

Query Match 28.6%; Score 16; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWM 12
 DB 5 YWM 7

RESULT 6
 UPAA_HUMAN STANDARD; PRT; 8 AA.
 ID UPAA_HUMAN
 AC P30096;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RT Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7, ITS MW IS: 12 KDa.
 DR SWISS-2DPAGE; P30096; HUMAN.
 FT NON TER 1
 FT VARIANT 5 5 F -> P.
 FT /FTID=VAR_000004.
 SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;
 Query Match 28.6%; Score 16; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.1e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IXLXYT 11
 DB 1 VILTFY 6

RESULT 7
 GON3_ONCKE STANDARD; PRT; 10 AA.
 ID GON3_ONCKE
 AC P20367; P81751;
 RC

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-
 DE RH III) (Luliberin III).
 GN GNRH3.
 OS Oncorhynchus keta (Chum salmon), and
 OS Clupea pallasii (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OC NCBI_TaxID=8018, 30724;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=O. keta;
 RX MEDLINE=83195140; PubMed=6341999;
 RA Sherwood N., Biden L., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RT Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 RN [2]
 RP SEQUENCE, AND FUNCTION.
 RC SPECIES=C. pallasii; TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650923;
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 RT hormones, including a novel form, from an ancient teleost, herring.";
 RT Endocrinology 141:505-512(2000).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 CC FOLLICLE-STIMULATING HORMONES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR PIR, A21114; A21114.
 DR InterPro: IPR02012; GNRH.
 DR Pfam: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 KM Hormone; Amidation; Hypothalamus.
 FT MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT AMIDATION.
 SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B4543 CRC64;
 Query Match 26.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWM 12
 DB 5 YGM 7

RESULT 8
 LPM_RHIME STANDARD; PRT; 14 AA.
 ID LPM_RHIME
 AC P18854;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRP operon leader peptide.
 GN TRP OR R02387.1 OR SMC02725.1;
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OC NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89255120; PubMed=2656657;
 RA Bae Y.M., Holmgren E., Crawford I.P.;
 RT "Rhizobium meliloti anthranilate synthase gene: cloning, sequence,
 RT and expression in Escherichia coli.";
 RL J. Bacteriol. 171:3471-3478(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;

RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
 RA Boletard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godle T., Goffeau A., Kahn D., Kias E., Lelure V., Masny D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Ransperger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.,
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT *Sinorhizobium meliloti* strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.
 CC -----
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 CC -----
 DR EMBL, M22983; -; NOT ANNOTATED_CDS.
 DR EMBL, AL591790; -; NOT ANNOTATED_CDS.
 DR PIR, A44515; A44515.
 DR Tyropan biosynthesis, leader peptide, Complete proteome.
 SQ SEQUENCE 14 AA; 1777 MW; 05BFD63BC52A7C80 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 YW 12
 Db 10 WW 12

RESULT 9
 DT NEPNO STANDARD; PRT; 9 AA.
 AC P24816;
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DE Gastrin/cholecystokinin-like peptide D1.
 OS Nephrops norvegicus (Norway lobster).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Decapoda; Pleocyemata;
 CC Astacidea; Nephropidae; Nephropidae; Nephrops.
 CC NCB1_TaxID=6829;
 RN (1)
 RP SEQUENCE.
 RC Tissue=stomach;
 RX MEDLINE=92082847; PubMed=1747388;
 RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.,
 RT "Structure and biological activity of crustacean gastrointestinal
 RT peptides identified with antibodies to gastrin/cholecystokinin";
 RL Biochimie 73:1233-1239(1991).
 CC -1- FUNCTION: MAY CONTROL DIGESTION PROCESS IN CRUSTACEANS.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR, A48398; A48398.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match 25.0%; Score 14; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YW 12
 Db 7 FW 8

RESULT 10
 UR2A_CATCO

ID UR2A_CATCO STANDARD; PRT; 12 AA.
 AC P04558;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin IIA (U-IIA) (UIIA).
 OS Catestomus commersoni (White sucker).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 CC Catestomidae; Catestomus.
 CC NCB1_TaxID=7971;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=84041959; PubMed=6138758;
 RA McMaster D., Lederis K.;
 RT "Isolation and amino acid sequence of two urotensin II peptides from
 RT *Catestomus commersoni* urophyses.";
 RL Peptides 4:367-373(1983).
 CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR.
 CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
 DR PIR, JS0423; JS0423.
 DR InterPro, IPR001483; Urotensin_II.
 DR Pfam, PF02083; Urotensin_II; 1.
 DR PROSITE, PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID
 SQ SEQUENCE 12 AA; 1336 MW; 969C76DBB879CEBA CRC64;

Query Match 25.0%; Score 14; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YW 12
 Db 7 FW 8

RESULT 11
 UR2B_CATCO STANDARD; PRT; 12 AA.
 AC P04559;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin IIB (U-IIB) (UIIB).
 OS Catestomus commersoni (White sucker).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 CC Catestomidae; Catestomus.
 CC NCB1_TaxID=7971;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=84041959; PubMed=6138758;
 RA McMaster D., Lederis K.;
 RT "Isolation and amino acid sequence of two urotensin II peptides from
 RT *Catestomus commersoni* urophyses.";
 RL Peptides 4:367-373(1983).
 CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR.
 CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
 DR PIR, JS0424; JS0424.
 DR InterPro, IPR001483; Urotensin_II.
 DR Pfam, PF02083; Urotensin_II; 1.
 DR PROSITE, PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID
 SQ SEQUENCE 12 AA; 1437 MW; 73961BDBB879CEBA CRC64;

Query Match 25.0%; Score 14; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 11 YW 12
 DB 7 FW 8

RESULT 12
 UR2B_CYPCA STANDARD; PRT; 12 AA.

AC P045EL;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II-beta.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 NCBI_Taxid=7962;
 RN [1]
 RP SEQUENCE.

RA Munekeata E., Ohnaka T., Ichikawa T., McMaster D., Lederis K.;
 RL (in) Rich D.H., Gross E. (eds.);
 RL Proceedings of the 7th American peptide symposium, pp.69-72,
 RL Pierce Chemical Co., Rockford IL. (1981).
 CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR.

CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

DR InterPro; IPR001483; Urotensin_II.

DR Pfam; PF02083; Urotensin_II; 1.

DR PROSITE; PS00984; UROTENSIN_II; 1.

KW Hormone.

FT DISULFID

FT VARIANT

SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;

Query Match 25.0%; Score 14; DB 1; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
 DB 7 FW 8

RESULT 13
 UR2_GILMI STANDARD; PRT; 12 AA.

AC P01147;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Urotensin II (U-II) (UII).

OS Gillichthys mirabilis (Long-jawed mudsnucker).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Gobioidae;

OC Gobiidae; Gillichthys.

NCBI_Taxid=8222;

RN [1]

RP SEQUENCE.

RA MEDLINE=81054904; PubMed=6107911;

RA Pearson D., Shively J.E., Clark B.R., Geschwind I.I., Barkley M.,

RA Nishio R., Bern H.A.;

RT "Urotensin II: a somatostatin-like peptide in the caudal

RT neurosecretory system of fishes.";

RL Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).

CC -1- FUNCTION: UROTENSIN IS FOUND IN THE OSOREGULATORY AND AS A
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR.
 CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

DR PIR; A01409; UOEN2.
 DR InterPro; IPR001483; Urotensin_II.
 DR Pfam; PF02083; Urotensin_II; 1.
 DR PROSITE; PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID

SQ SEQUENCE 12 AA; 1364 MW; 968BF8962679CEBA CRC64;
 Query Match 25.0%; Score 14; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
 DB 7 FW 8

RESULT 14
 UR2_POLSP STANDARD; PRT; 12 AA.

AC P81022;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Urotensin II (U-II) (UII).

OS Polyodon spathula (North American paddlefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;

OC Polyodon.

NCBI_Taxid=7913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spinal cord;

RX MEDLINE=86051494; PubMed=8536944;

RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;

RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea

RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon

RT spathula).";

RL Gen. Comp. Endocrinol. 99:323-332(1995).

CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH

CC MUSCLE STIMULATION.

CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

DR InterPro; IPR001483; Urotensin_II.

DR Pfam; PF02083; Urotensin_II; 1.

DR PROSITE; PS00984; UROTENSIN_II; 1.

KW Hormone.

FT DISULFID

SQ SEQUENCE 12 AA; 1410 MW; 751E9DBB879CEBB CRC64;

Query Match 25.0%; Score 14; DB 1; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
 DB 7 FW 8

RESULT 15
 UR2_SCYCA STANDARD; PRT; 12 AA.

AC P35490;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Urotensin II (U-II) (UII).

OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;

SCyliorhinidae; Scyliorhinus.

NCBI_Taxid=7830;

RN [1]

RP SEQUENCE
RC TISSUE=Spinal cord; PubMed=1620290;
RX MEDLINE=92319231; PubMed=1620290;
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazon N.;
RT "Purification and characterization of urotensin II and parvalbumin
from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
RL Neuroendocrinology 55:230-235(1992).
CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
DR InterPro: IPR001483; Uroensin_II.
DR Pfam: PF02083; Uroensin_II; 1.
DR PROSITE; PS00984; UROSENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; 804729F9D579CEBA CRC64;

Query Match 25.0%; Score 14; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YW 12
: 1
DB 7 FW 8

Search completed: May 5, 2003, 14:12:08
Job time : 13 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:09:26 ; Search time 82 Seconds
(without alignments)
35.179 Million cell updates/sec

Title: US-09-742-148a-3
Perfect score: 56
Sequence: 1 RXXLRILXLYWXS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 2683

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	41.1	9	Q94XE6	Q94XE6 tectocoris
2	23	41.1	9	Q94NB2	Q94NB2 microcebus
3	23	41.1	9	Q94NB1	Q94NB1 microcebus
4	23	41.1	9	Q94NB0	Q94NB0 microcebus
5	23	41.1	9	Q94NA9	Q94NA9 daubentonla
6	23	41.1	13	Q99783	Q99783 caprimulgus
7	20	35.7	12	Q9UR28	Q9UR28 filobasidia
8	19	33.9	10	Q9PRU9	Q9PRU9 sparus aura
9	18	32.1	9	Q65711	Q65711 berne virus
10	18	32.1	12	Q91CES	Q91CES human immun
11	18	32.1	13	Q16406	Q16406 homo sapien
12	18	32.1	13	Q9THR8	Q9THR8 bryopsis sp
13	17	30.4	11	Q04131	Q04131 lycopersico
14	17	30.4	14	Q9MT61	Q9MT61 allium cepa
15	17	30.4	14	Q9MRV1	Q9MRV1 allium sativ
16	17	30.4	14	Q9MRV4	Q9MRV4 allium porr

17	17	30.4	14	8	Q9MT8	Q9MT8 aloa vera (
18	17	30.4	14	11	Q9JHK8	Q9JHK8 mus musculu
19	16	28.6	8	4	Q15888	Q15888 homo sapien
20	16	28.6	13	8	Q94RE2	Q94RE2 leptomonas
21	16	28.6	13	11	Q9QM45	Q9QM45 rectus sp.
22	15	26.8	8	8	Q94VB5	Q94VB5 varanus sal
23	15	26.8	8	8	Q94VB2	Q94VB2 varanus sal
24	15	26.8	8	8	Q94VA7	Q94VA7 varanus sal
25	15	26.8	9	8	Q94VC6	Q94VC6 varanus pil
26	15	26.8	10	8	Q94VP5	Q94VP5 varanus oli
27	15	26.8	12	2	Q93UT4	Q93UT4 escherichia
28	15	26.8	12	10	Q9S8FO	Q9S8FO zea mays (m
29	15	26.8	12	11	Q61331	Q61331 mus musculu
30	15	26.8	13	6	Q18890	Q18890 atelea belz
31	15	26.8	14	12	Q9PY99	Q9PY99 murine hepa
32	15	26.8	14	12	Q67112	Q67112 influenza vi
33	14	25.0	8	4	Q15890	Q15890 homo sapien
34	14	25.0	8	6	Q95M23	Q95M23 sub scrota
35	14	25.0	8	8	Q94VB2	Q94VB2 varanus yuw
36	14	25.0	8	11	Q62721	Q62721 rattus norv
37	14	25.0	9	4	Q9H326	Q9H326 homo sapien
38	14	25.0	9	8	Q94V10	Q94V10 varanus gfg
39	14	25.0	10	8	Q94VG5	Q94VG5 varanus gri
40	14	25.0	10	8	Q8SHN1	Q8SHN1 bradypodion
41	14	25.0	11	4	Q8TD48	Q8TD48 homo sapien
42	14	25.0	11	7	Q77884	Q77884 oreochromis
43	14	25.0	11	7	Q77885	Q77885 oreochromis
44	14	25.0	11	7	Q77894	Q77894 oreochromis
45	14	25.0	11	7	Q77895	Q77895 oreochromis

ALIGNMENTS

RESULT 1

Q94XE6 PRELIMINARY; PRT; 9 AA.

AC Q94XE6; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Cytochrome c oxidase subunit III (Fragment).

GN COX3.

OS Tectocoris diophtalmus (cotton harlequin bug).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;

OC Heteroptera; Pentheteroptera; Pentatomomorpha; Pentatomidae;

OC Pentatomidae; Tectocoris.

OX NCBI_TaxID=159956;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21396409; PubMed=11504862;

RA Shao R., Campbell N.J.H., Schmidt E.R., Barker S.C.;

RT "Increased rate of gene rearrangement in the mitochondrial genomes of

RT three orders of hemipteroid insects";

RL Mol. Biol. Evol. 18:1828-1832(2001).

DR EMBL; AF335990; AAKS5283.1; .

KW Mitochondrion.

FT NON TER

SQ SEQUENCE 9 AA; 1206 MW; A2C5636B5041A6 CRC64;

Query Match 41.1%; Score 23; DB 8; Length 9;

Best Local Similarity 60.0%; Pred. No. 6.7e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14

DB 5 YWGS 9

RESULT 2

Q94NB2

```
ID 094NB2 PRELIMINARY; PRT; 9 AA.
AC 094NB2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Cytochrome oxidase subunit III (fragment).
GN COI11.
OS Microcebus murinus (Lesser mouse lemur).
OC Microchondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JP285, JP288, JP292, JP308, AND JP313;
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
DR EMBL; AF224624; AAK70547.1; -.
DR EMBL; AF224625; AAK70551.1; -.
DR EMBL; AF224626; AAK70555.1; -.
DR EMBL; AF224627; AAK70559.1; -.
DR EMBL; AF224628; AAK70563.1; -.
DR EMBL; AF224629; AAK70567.1; -.
KW Mitochondrion.
FT NON TER. 1
SQ SEQUENCE 9 AA; 1160 MW; DSC563636B5045A2 CRC64;
```

Query Match

Best Local Similarity 41.1%; Score 23; DB 8; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 YWXS 14
Db 5 YWGS 9

```
RESULT 3
ID 094NB1 PRELIMINARY; PRT; 9 AA.
AC 094NB1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome oxidase subunit III (fragment).
GN COI11.
OS Microcebus ravelobensis.
OC Microchondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122231;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JP299, AND JP301;
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
DR EMBL; AF224630; AAK70571.1; -.
DR EMBL; AF224631; AAK70575.1; -.
KW Mitochondrion.
FT NON TER. 1
SQ SEQUENCE 9 AA; 1160 MW; DSC563636B5045A2 CRC64;
```

Query Match 41.1%; Score 23; DB 8; Length 9;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 YWXS 14
Db 5 YWGS 9

```
RESULT 4
ID 094NB0 PRELIMINARY; PRT; 9 AA.
AC 094NB0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Cytochrome oxidase subunit III (fragment).
GN COI11.
OS Microcebus rufus (brown mouse lemur).
OC Microchondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JP309, JP315, JP316, AND JP317;
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
DR EMBL; AF224636; AAK70595.1; -.
DR EMBL; AF224637; AAK70599.1; -.
DR EMBL; AF224638; AAK70603.1; -.
DR EMBL; AF224639; AAK70607.1; -.
KW Mitochondrion.
FT NON TER. 1
SQ SEQUENCE 9 AA; 1160 MW; DSC563636B5045A2 CRC64;
```

Query Match

Best Local Similarity 41.1%; Score 23; DB 8; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 YWXS 14
Db 5 YWGS 9

```
RESULT 5
ID 094NA9 PRELIMINARY; PRT; 9 AA.
AC 094NA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome oxidase subunit III (fragment).
GN COI11.
OS Daubentonia madagascariensis (Aye-aye).
OC Microchondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;
OC Daubentonia.
OX NCBI_TaxID=31869;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JP119, AND JP120;
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
DR EMBL; AF224641; AAK70615.1; -.
DR EMBL; AF224642; AAK70619.1; -.
KW Mitochondrion.
FT NON TER. 1
SQ SEQUENCE 9 AA; 1160 MW; DSC563636B5045A2 CRC64;
```

Query Match 41.1%; Score 23; DB 8; Length 9;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14
 | : |
 Db 5 YWGS 9

RESULT 6

Q99783 PRELIMINARY; PRT; 13 AA.

AC Q99783; 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cytochrome oxidase subunit III (Fragment).
 OS Caprimulgus vociferus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Caprimulgiformes; Caprimulgidae;
 OC Caprimulginae; Caprimulgus.
 NCBI_TaxID=57400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT Mindell D.P., Sorenson M.D., Dimcheff D.E.;
 RT "An extra nucleotide is not translated in mitochondrial ND3 of some
 RT birds and turtles.";
 RT Mol. Biol. Evol. 15:1568-1571(1998).
 DR EMBL; AF076372; AAC83312.1; -
 DR InterPro; IPR000298; Cyto_oxide_III.
 DR Pfam; PF00510; COX3; 1.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1766 MW; A29B49E3549B41A6 CRC64;
 Query Match 41.1%; Score 23; DB 8; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14
 | : |
 Db 9 YWGS 13

RESULT 7

Q9UR28 PRELIMINARY; PRT; 12 AA.

AC Q9UR28; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE STE12 alpha (Fragment).
 OS STE12ALPHA.
 OS Filobasidiella bacillisporea.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 NCBI_TaxID=37769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CSS5757, 1408, 571 146, BAL 21, AND E 316;
 RX MEDLINE=99380307; PubMed=10449476;
 RA Halliday C.L., Bul T., Krockenberger M., Malik R., Ellis D.H.,
 RA Carter D.A.;
 RA "Presence of alpha and a mating types in environmental and clinical
 RT collections of Cryptococcus neoformans var. gattii strains from
 RT Australia.";
 RT J. Clin. Microbiol. 37:2920-2926(1999).
 RL EMBL; AF155346; AAF20371.1; -
 DR EMBL; AF155342; AAF20367.1; -
 DR EMBL; AF155343; AAF20368.1; -
 DR EMBL; AF155344; AAF20369.1; -

DR EMBL; AF155345; AAF20370.1; -
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1477 MW; 460BA17A8A729C7 CRC64;

Query Match 35.7%; Score 20; DB 3; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RIXLXY 11
 | : |
 Db 4 RLFTFY 10

RESULT 8

Q9PRU9 PRELIMINARY; PRT; 10 AA.

AC Q9PRU9; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Gonadotropin-releasing hormone, SBGNRH-1.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95083645; PubMed=7991588;
 RA Powell J.F., Zohar Y., Ellicur A., Park M., Fischer W.H., Craig A.G.,
 RA Rivier J.E., Lovejoy D.A., Sherwood N.M.;
 RT "Three forms of gonadotropin-releasing hormone characterized from
 RT brains of one species.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).
 SQ SEQUENCE 10 AA; 1132 MW; 81566865AB587735 CRC64;

Query Match 33.9%; Score 19; DB 13; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 LXYYW 12
 | : |
 Db 4 LGYSW 8

RESULT 9

Q65711 PRELIMINARY; PRT; 9 AA.

AC Q65711; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
 DE ORF3 (Fragment).
 OS Berne virus (BEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Torovirus.
 NCBI_TaxID=11156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90080137; PubMed=2293666;
 RA Snijder E.J., Horzinek M.C., Spaan W.J.M.;
 RT "A 3'-terminal nested set of independently transcribed mRNAs is
 RT generated during Berne virus replication.";
 RT J. Virol. 64:331-338(1990).
 DR EMBL; M33502; AAA42817.1; -
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1234 MW; DBE736B5451AB19 CRC64;

Query Match 32.1%; Score 18; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12
DB 6 YW 7

RESULT 10

ID O9ICES PRELIMINARY; PRT; 12 AA.
AC O9ICES;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=546CP-H7, 546CP-E4, AND 546CP-F5;
RA Gartner-S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into brain."
RL J. Neurovirol. 0:0-0(2000).
DR EMBL; AF217153; AAF75497.1; -;
DR EMBL; AF217154; AAF75495.1; -;
DR EMBL; AF217154; AAF75496.1; -;
SQ SEQUENCE 12 AA; 1636 MW; 7ED6A2917A24005B CRC64;

Query Match 32.1%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12
DB 10 YW 11

RESULT 11

ID O16406 PRELIMINARY; PRT; 13 AA.
AC O16406;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)
DE GHRH-R protein (Fragment).
GN GHRH-R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96001284; PubMed=7559877;
RA Hashimoto K., Koga M., Motomura T., Kasayama S., Kouhara H.,
RA Ohnishi T., Arita N., Hayakawa T., Sato B., Kishimoto T.;
RT "Identification of alternatively spliced messenger ribonucleic acid RT encoding truncated growth hormone-releasing hormone receptor in human pituitary adenoma."
RL J. Clin. Endocrinol. Metab. 80:2933-2939(1995).
DR EMBL; S79912; AAD14318.1; -;
FT NON_TER 1
SQ SEQUENCE 13 AA; 1612 MW; CB19D7D255D6362 CRC64;

Query Match 32.1%; Score 18; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12
DB 9 YW 10

RESULT 12

ID O9THR8 PRELIMINARY; PRT; 13 AA.
AC O9THR8;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE PbsH (Fragment).
GN PbsH.
OS Bryopsis sp. A.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103784;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98-02-01;
RA Kreilwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North Atlantic and Caribbean based on Coding and Non-coding sequences of the RT Chloroplast pbsH Operon."
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF170413; AAD56858.1; -;
KW Chloroplast.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1785 MW; 3F9A1C3E247D0323 CRC64;

Query Match 32.1%; Score 18; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 YW 12
DB 5 YW 6

RESULT 13

ID O04131 PRELIMINARY; PRT; 11 AA.
AC O04131;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIK-RED; TISSUE=PERICARP;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit: interactions with fruit development, ethylene and light."
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -;
FT NON_TER 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 30.4%; Score 17; DB 10; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 LXXY 11
DB 8 LDYX 11

RESULT 14

Q9WT61
 ID Q9WT61 PRELIMINARY; PRT; 14 AA.
 AC Q9WT61;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PSI 9 kDa protein (Fragment).
 GN PSAC.
 OS Allium cepa (Onion).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
 OC Allium.
 OX NCBI_TaxID=4679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
 RT "Conservation of the start codon by editing in nhd-encoded
 transcripts is not restricted to dicotyledonous plants."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBS databases.
 DR EMBL; AJ278350; CAB96183.1; -.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Query Match 30.4%; Score 17; DB 8; Length 14;
 Best Local Similarity 66.7%; Pred. No. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 YW 12
 | |
 Db 1 YLW 3

RESULT 15
 Q9MRV1
 ID Q9MRV1 PRELIMINARY; PRT; 14 AA.
 AC Q9MRV1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PSI 9 kDa protein (Fragment).
 GN PSAC.
 OS Allium sativum (Garlic).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
 OC Allium.
 OX NCBI_TaxID=4682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
 RT "Conservation of the start codon by editing in nhd-encoded
 transcripts is not restricted to dicotyledonous plants."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBS databases.
 DR EMBL; AJ278351; CAB96187.1; -.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Query Match 30.4%; Score 17; DB 8; Length 14;
 Best Local Similarity 66.7%; Pred. No. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 YW 12
 | |
 Db 1 YLW 3

Search completed: May 5, 2003, 14:13:39
 Job time : 85 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:03:05 ; Search time 34 Seconds
(without alignments)
54.868 Million cell updates/sec

Title: US-09-742-148A-3

Sequence: 1 RXXLRIXLYYWS 14

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 228063

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Minimum DB seq length: 0
Maximum DB seq length: 14
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_101002:*

23	/S1D2/gcgdata/genseq/genseqp-emb1/A11981.DAT *
24	/S1D2/gcgdata/genseq/genseqp-emb1/A11980.DAT *
25	/S1D2/gcgdata/genseq/genseqp-emb1/A11981.DAT *
26	/S1D2/gcgdata/genseq/genseqp-emb1/A11982.DAT *
27	/S1D2/gcgdata/genseq/genseqp-emb1/A11983.DAT *
28	/S1D2/gcgdata/genseq/genseqp-emb1/A11984.DAT *
29	/S1D2/gcgdata/genseq/genseqp-emb1/A11985.DAT *
30	/S1D2/gcgdata/genseq/genseqp-emb1/A11986.DAT *
31	/S1D2/gcgdata/genseq/genseqp-emb1/A11987.DAT *
32	/S1D2/gcgdata/genseq/genseqp-emb1/A11988.DAT *
33	/S1D2/gcgdata/genseq/genseqp-emb1/A11989.DAT *
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35	/S1D2/gcgdata/genseq/genseqp-emb1/A11991.DAT *
36	/S1D2/gcgdata/genseq/genseqp-emb1/A11992.DAT *
37	/S1D2/gcgdata/genseq/genseqp-emb1/A11993.DAT *
38	/S1D2/gcgdata/genseq/genseqp-emb1/A11994.DAT *
39	/S1D2/gcgdata/genseq/genseqp-emb1/A11995.DAT *
40	/S1D2/gcgdata/genseq/genseqp-emb1/A11996.DAT *
41	/S1D2/gcgdata/genseq/genseqp-emb1/A11997.DAT *
42	/S1D2/gcgdata/genseq/genseqp-emb1/A11998.DAT *
43	/S1D2/gcgdata/genseq/genseqp-emb1/A11999.DAT *
44	/S1D2/gcgdata/genseq/genseqp-emb1/A12000.DAT *
45	/S1D2/gcgdata/genseq/genseqp-emb1/A12001.DAT *
46	/S1D2/gcgdata/genseq/genseqp-emb1/A12002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	82.1	14	17	AAW07511	Generic T-cell mol
2	45	82.1	14	22	AAW59403	Human Class I HLA
3	41	73.2	10	22	AA772482	Immunosuppressive
4	41	73.2	10	22	AAW59457	Human Class I HLA
5	41	73.2	14	22	AAW59417	Human Class I HLA
6	41	73.2	14	22	AAW59418	Human Class I HLA
7	35	62.5	13	22	AAW59419	Human Class I HLA
8	31	55.4	13	22	AAW59420	Human Class I HLA
9	31	55.4	13	22	AAW59421	Human Class I HLA
10	30	53.6	14	22	AAW59416	Human Class I HLA

11	28	50.0	5	18	AAW194005
12	28	50.0	10	18	AAW194006
13	28	50.0	11	20	AAW061551
14	28	50.0	13	20	AAW351805
15	28	50.0	13	20	AAW899595
16	28	50.0	13	23	AAE1652262
17	28	50.0	14	18	AAW194003
18	27	48.2	10	22	AAW83107
19	27	48.2	14	22	AAW544310
20	27	48.2	14	22	AAW594303
21	27	48.2	14	22	AAW594431
22	27	48.2	14	22	AAW594441
23	26	46.4	10	14	AAW412018
24	26	46.4	10	16	AAW954137
25	26	46.4	10	16	AAW954422
26	26	46.4	10	16	AAW830606
27	26	46.4	10	16	AAW830994
28	26	46.4	10	17	AAW075121
29	26	46.4	10	17	AAW075121
30	26	46.4	10	19	AAW33784
31	26	46.4	10	19	AAW33787
32	26	46.4	10	19	AAW472656
33	26	46.4	10	19	AAW472656
34	26	46.4	10	21	AAW542131
35	26	46.4	10	21	AAW267878
36	26	46.4	10	22	AAW72477
37	26	46.4	10	22	AAW724807
38	26	46.4	13	21	AAW560003
39	26	46.4	14	22	AAW594004
40	26	46.4	14	22	AAW594007
41	26	46.4	14	22	AAW594511
42	26	46.4	14	22	AAW594545
43	26	46.4	3	22	AAW594007
44	25	44.6	4	22	AAW594007
45	25	44.6	5	18	AAW24544

ALIGNMENTS

RESULT 1	
AAW07511	
ID	AAW07511 standard; peptide; 14 AA.
XX	
AC	AAW07511;
XX	
DT	04-AUG-1997 (first entry)
XX	
DE	Generic T-cell modulating peptide #2.
XX	
KW	T-cell modulator; autoimmune disease; tissue destruction; alpha-domain;
KW	mammal; major histocompatibility complex; MHC class I; antigen; perforin;
KW	insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW	rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW	thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW	autologous target cell; cytokine release; T cell activation; therapy;
XX	generic peptide.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	Misc-difference 2
FT	/label= Val, Glu
FT	Misc-difference 7
FT	/label= Ala, Leu
FT	Misc-difference 9
FT	/label= Arg, Leu
FT	Misc-difference 13
FT	/label= Gln, Asp
XX	
PN	W09635443-A1.
XX	
PD	14-NOV-1996

XX 05-APR-1996; 96MO-US04710.
XX 12-MAY-1995; 95US-0440504.
XX (SANG-) SANGSTAT MEDICAL CORP.
XX Buelow R;
XX WPI; 1996-518410/51.
XX
XX Treatment of auto-immune disease by admin. of peptide(e) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset
PT of clinical symptoms of insulin dependent diabetes by modulating T
PT cell mediated attack on target cells
XX
XX Claim 2; Page 20; 24pp; English.
XX
XX AAM07510 and AAM07511 represent generic T-cell modulating peptides.
CC These sequences, and specific peptides created from them (such as
CC AAM07512-W07518) can be used in the method of the invention. The method
CC is for affecting the course of an autoimmune disease involving T-cell
CC mediated destruction of tissue in mammals. These sequences are based on
CC the alpha1-domains of the major histocompatibility complex (MHC)
CC antigens. These peptides are used especially to treat insulin-dependent
CC diabetes mellitus, preferably being administered during the pre-clinical
CC stage to delay onset of the disease. Other diseases that can be treated
CC are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus
CC vulgaris, Sjogren's disease, thyroid disease, Hashimoto's thyroiditis,
CC myasthenia gravis, etc. The peptides modulate T-cell mediated attack on
CC autologous target cells, and may also reduce inflammation, swelling, and
CC release of cytokines, perforins, granzymes etc. associated with T cell
CC activation.
XX
XX
SO Sequence 14 AA;
Query Match 82.1%; Score 46; DB 17; Length 14;
Best Local Similarity 92.9%; Pred. No. 0.035;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RXLRLIXLXYWXS 14
Db 1 RXBLRLIXLXYWXS 14
RESULT 2
AAB59403
ID AAB59403 standard; Peptide; 14 AA.
XX
XX AAB59403;
XX
XX 22-MAR-2001 (first entry)
XX
XX Human Class I HLA-B alpha1-domain-derived peptide #3.
XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
XX cytotoxic T cell activation inhibition; cell transplantation;
XX natural killer cell activation inhibition; organ transplantation.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH MISC-difference 2 /label= Val, Glu
FT MISC-difference 3 /label= Asn, Asp
FT MISC-difference 7 /label= Ala, Leu
FT MISC-difference 9 /label= Arg, Glu
FT MISC-difference 13 /label= Gln, Asp

XX US6162434-A.
XX 19-DEC-2000.
XX 03-MAY-1995; 95US-0433613.
XX 03-MAY-1995; 95US-0433613.
XX (SANG-) SANGSTAT MEDICAL CORP.
XX Buelow R;
XX WPI; 2001-111720/12.
XX
XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
XX Claim 8; Column 37; 20pp; English.
XX
XX The present sequence is a peptide which may be used in a method for
CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
CC cells. The method involves combining the cells with a compound
CC comprising an oligopeptide of at least 6 amino acids comprising a
CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
CC including amino acids 84-86, where amino acids 84-86 are YW.
CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.
XX
XX
SO Sequence 14 AA;
Query Match 82.1%; Score 46; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXLRLIXLXYWXS 14
Db 1 RXLRLIXLXYWXS 14
RESULT 3
AA72482
ID AA72482 standard; peptide; 10 AA.
XX
XX AA72482;
XX
XX 24-APR-2001 (first entry)
XX
XX Immunosuppressive peptide, P15, to prevent allograft rejection.
XX Immunosuppressive; allograft rejection; topological parameter;
XX physico-chemical parameter; in silico screening; pharmaceutical;
XX cosmetic; agrochemical; biomaterial; veterinary application.
XX
XX Unidentified.
OS
XX WO200079263-A2.
XX
XX 28-DEC-2000.
XX
XX 15-MAY-2000; 2000MO-EP04338.
XX
XX 18-JUN-1999; 99EP-0401526.
XX (SYNT-) SYNT:EM SA.
XX
XX Lahana R, Clair P, Yaari A;
XX
XX WPI; 2001-091623/10.
XX
XX

XX Identifying active candidate molecules on the basis of selected
PT physico-chemical parameters, for in silico screening of compounds
PT useful in pharmaceuticals, cosmetics, veterinary applications and
PT agrochemicals -
XX
XX Disclosure; Page 38; 55pp; English.
XX
XX The present invention relates to a method for identifying
CC physico-chemical and/or topological parameters associated with biological
CC activity. The method involves selecting the first subset from
CC predetermined set of physico-chemical parameters, determining their value
CC of function, and selecting the second subset from physico-chemical
CC parameters based on the values of function, such that each second subset
CC is more closely associated with the activity than the first subset. The
CC selected physico-chemical parameters are useful for developing criteria
CC for screening candidate molecules and are suitable for use in silico
CC screening of compounds. The compounds may be used in pharmaceuticals,
CC cosmetics, agrochemicals, biomaterials and in veterinary applications. It
CC is also useful as an antibiotic or antifungal agent. The present
CC sequence is an immunosuppressive peptide, P15, identified by in silico
CC screening. The immunosuppressive activity of the peptide that prevents
CC allograft rejection is tested in a heterotopic allograft model of mouse.
XX
SQ Sequence 10 AA;

Query Match 73.2%; Score 41; DB 22; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.21; 2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LRILXLYYW 12
||| |||
Db 2 LRILXLYYW 10

RESULT 4
AAB59457
ID AAB59457 standard; Peptide; 10 AA.
XX
AC AAB59457;
XX
DT 22-MAR-2001 (first entry)
XX
XX Human Class I HLA-B alpha1-domain-derived peptide #57.
DE
XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
KM cytotoxic T cell activation inhibition; cell transplantation;
KW natural killer cell activation inhibition; organ transplantation.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX US6162434-A.
XX
XX 19-DEC-2000.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX (SANG-) SANGSTAT MEDICAL CORP.
XX
XX Buelow R;
XX
XX WPI; 2001-111720/12.
XX
XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
XX Claim 12; Column 38, 20pp; English.
XX
XX The present sequence is a peptide which may be used in a method for

CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
CC cells. The method involves combining the cells with a compound
CC comprising an oligopeptide of at least 6 amino acids comprising a
CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
CC including amino acids 84-86, where amino acids 84-86 are YW.
CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.
XX
SQ Sequence 10 AA;

Query Match 73.2%; Score 41; DB 22; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.21; 2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LRILXLYYW 12
||| |||
Db 2 LRILXLYYW 10

RESULT 5
AAB59417
ID AAB59417 standard; Peptide; 14 AA.
XX
AC AAB59417;
XX
DT 22-MAR-2001 (first entry)
XX
XX Human Class I HLA-B alpha1-domain-derived peptide #17.
DE
XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
KM cytotoxic T cell activation inhibition; cell transplantation;
KW natural killer cell activation inhibition; organ transplantation.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX US6162434-A.
XX
XX 19-DEC-2000.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX 03-MAY-1995; 95US-0433613.
XX
XX (SANG-) SANGSTAT MEDICAL CORP.
XX
XX Buelow R;
XX
XX WPI; 2001-111720/12.
XX
XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
PT cells involves combining cells with compound comprising oligopeptide
PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
XX
XX Disclosure; Column 7-8, 20pp; English.
XX
XX The present sequence is a peptide which may be used in a method for
CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
CC cells. The method involves combining the cells with a compound
CC comprising an oligopeptide of at least 6 amino acids comprising a
CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
CC including amino acids 84-86, where amino acids 84-86 are YW.
CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.
XX
XX Sequence 14 AA;
SQ

Query Match 73.2%; Score 41; DB 22; Length 14;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 LRIKLYYW 12
 |||||
 DB 6 LRIALRYW 14

RESULT 6
 AAB59418
 ID AAB59418 standard; Peptide; 14 AA.

AC AAB59418;
 XX
 AC AAB59418;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Human Class I HLA-B alpha1-domain-derived peptide #18.

XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.

XX Homo sapiens.
 OS Synthetic.

XX US6162434-A.
 XX
 PD 19-DEC-2000.

XX 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.

XX (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R;
 XX
 DR WPI; 2001-111720/12.

XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
 XX
 PS Disclosure; Column 7-8; 20pp; English.

XX The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
 CC including amino acids 84-86, where amino acids 84-86 are YW.
 CC The method is useful for transplanting a donor mammalian organ or cells
 CC to a mammalian recipient. The organ or cells are combined with the
 CC compound prior to implanting in the mammalian recipient, or the compound
 CC may be administered to the mammalian recipient in a period extending
 CC from prior to implanting the donor organ or cells.

XX Sequence 14 AA;

Query Match 73.2%; Score 41; DB 22; Length 14;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 LRIKLYYW 12
 |||||
 DB 5 LRIALRYW 13

RESULT 7
 AAB59419
 ID AAB59419 standard; Peptide; 13 AA.

AC AAB59419;
 XX
 DT 22-MAR-2001 (first entry)
 XX

DE Human Class I HLA-B alpha1-domain-derived peptide #19.

XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.

XX Homo sapiens.
 OS Synthetic.

XX US6162434-A.
 XX
 PD 19-DEC-2000.

XX 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.

XX (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buelow R;
 XX
 DR WPI; 2001-111720/12.

XX Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha1 domain
 XX
 PS Disclosure; Column 7-8; 20pp; English.

XX The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha1 domain
 CC including amino acids 84-86, where amino acids 84-86 are YW.
 CC The method is useful for transplanting a donor mammalian organ or cells
 CC to a mammalian recipient. The organ or cells are combined with the
 CC compound prior to implanting in the mammalian recipient, or the compound
 CC may be administered to the mammalian recipient in a period extending
 CC from prior to implanting the donor organ or cells.

XX Sequence 13 AA;

Query Match 62.5%; Score 35; DB 22; Length 13;
 Best Local Similarity 66.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 IXLXYWXS 14
 |||||
 DB 5 IALRYWDS 13

RESULT 8
 AAB59420
 ID AAB59420 standard; Peptide; 13 AA.

AC AAB59420;
 XX
 DT 22-MAR-2001 (first entry)
 XX

DE Human Class I HLA-B alpha1-domain-derived peptide #20.

XX Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.

XX Homo sapiens.
 OS Synthetic.

PN US6162434-A.
 XX
 PD 19-DEC-2000.
 XX
 PF 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buejow R;
 DR WPI; 2001-111720/12.
 PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha domain
 XX
 PS Disclosure; Column 9-10; 20pp; English.
 XX
 CC The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha domain
 CC including amino acids 84-86, where amino acids 84-86 are YYW.
 CC The method is useful for transplanting a donor mammalian organ or cells
 CC to a mammalian recipient. The organ or cells are combined with the
 CC compound prior to implanting in the mammalian recipient, or the compound
 CC may be administered to the mammalian recipient in a period extending
 CC from prior to implanting the donor organ or cells.
 CC
 SQ Sequence 13 AA;
 Query Match 55.4%; Score 31; DB 22; Length 13;
 Best Local Similarity 71.4%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 LKYYWXS 14
 Db 6 LKYYWXS 12
 RESULT 9
 AAB59421
 ID AAB59421 standard; Peptide; 13 AA.
 XX
 AC AAB59421;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Human Class I HLA-B alpha1-domain-derived peptide #21.
 XX
 KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN US6162434-A.
 XX
 PD 19-DEC-2000.
 XX
 PF 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buejow R;
 DR WPI; 2001-111720/12.

XX
 PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha domain
 XX
 PS Disclosure; Column 9-10; 20pp; English.
 XX
 CC The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha domain
 CC including amino acids 84-86, where amino acids 84-86 are YYW.
 CC The method is useful for transplanting a donor mammalian organ or cells
 CC to a mammalian recipient. The organ or cells are combined with the
 CC compound prior to implanting in the mammalian recipient, or the compound
 CC may be administered to the mammalian recipient in a period extending
 CC from prior to implanting the donor organ or cells.
 CC
 SQ Sequence 13 AA;
 Query Match 55.4%; Score 31; DB 22; Length 13;
 Best Local Similarity 71.4%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 LKYYWXS 14
 Db 5 LKYYWXS 11
 RESULT 10
 AAB59416
 ID AAB59416 standard; Peptide; 14 AA.
 XX
 AC AAB59416;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Human Class I HLA-B alpha1-domain-derived peptide #16.
 XX
 KW Human; human leukocyte antigen-B; HLA-B; immunosuppressive;
 KW cytotoxic T cell activation inhibition; cell transplantation;
 KW natural killer cell activation inhibition; organ transplantation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN US6162434-A.
 XX
 PD 19-DEC-2000.
 XX
 PF 03-MAY-1995; 95US-0433613.
 XX
 PR 03-MAY-1995; 95US-0433613.
 XX
 PA (SANG-) SANGSTAT MEDICAL CORP.
 XX
 PI Buejow R;
 DR WPI; 2001-111720/12.
 PT Inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 PT cells involves combining cells with compound comprising oligopeptide
 PT with contiguous sequence of human leukocyte antigen-B alpha domain
 XX
 PS Disclosure; Column 7-8; 20pp; English.
 XX
 CC The present sequence is a peptide which may be used in a method for
 CC inhibiting activation of cytotoxic T lymphocytes and/or natural killer
 CC cells. The method involves combining the cells with a compound
 CC comprising an oligopeptide of at least 6 amino acids comprising a
 CC contiguous sequence of a human leukocyte antigen (HLA)-B alpha domain
 CC including amino acids 84-86, where amino acids 84-86 are YYW.

CC The method is useful for transplanting a donor mammalian organ or cells
CC to a mammalian recipient. The organ or cells are combined with the
CC compound prior to implanting in the mammalian recipient, or the compound
CC may be administered to the mammalian recipient in a period extending
CC from prior to implanting the donor organ or cells.

XX
SQ Sequence 14 AA;

Query Match 53.6%; Score 30; DB 22; Length 14;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIKLXY 11
DB 7 LRIKLRY 14

RESULT 11:

AAW19405
ID AAW19405 standard; peptide; 5 AA.

XX
AC AAW19405;

DT 04-SEP-1997 (first entry)

DE Tissue factor peptide Hu#156-160 from human.

XX TF; factor X; factor VIIa; inhibitor; blood clotting;

KW coagulation; human.

XX Homo sapiens.

OS
PN WO9640779-A1.

XX
PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-GB01363.

XX 07-JUN-1995; 95US-0479223.

XX (MATT/) MATTHEWS D P.

PA (NYCO-) NYCOMED IMAGING AS.

PI Arbo B, Fischer P, Sakariassen KS, Oerning L;

XX WPI; 1997-052236/05.

PT Rabbit and mouse Tissue Factor-derived peptide(s) - useful for
PT inhibiting blood coagulation in humans

XX Disclosure; Page 7; 22pp; English.

XX The present sequence represents a peptide fragment Hu#156-160
XX corresponding to residues 156-160 of human tissue factor (TF).

CC The peptide sequence contains a putative Factor X binding site.

CC The peptide is an inhibitor of TF-dependent coagulation in humans,
CC specifically the binding of TF-factor VIIa to factor X. It is useful
CC for treating or preventing blood clotting disorders or associated
CC problems in humans.

XX
SQ Sequence 5 AA;

Query Match 50.0%; Score 28; DB 18; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YVWXS 14
DB 1 YVWXS 5

RESULT 12

AAW19404

ID AAW19404 standard; peptide; 10 AA.

XX
AC AAW19404;

DT 04-SEP-1997 (first entry)

DE Tissue factor peptide Hu#154-163 from human.

XX TF; factor X; factor VIIa; inhibitor; blood clotting;

KW coagulation; human.

XX Homo sapiens.

OS
PN WO9640779-A1.

XX
PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-GB01363.

XX 07-JUN-1995; 95US-0479223.

XX (MATT/) MATTHEWS D P.

PA (NYCO-) NYCOMED IMAGING AS.

PI Arbo B, Fischer P, Sakariassen KS, Oerning L;

XX WPI; 1997-052236/05.

PT Rabbit and mouse Tissue Factor-derived peptide(s) - useful for
PT inhibiting blood coagulation in humans

XX Example 1; Page 13; 22pp; English.

XX The present sequence represents a peptide fragment Hu#154-163
XX corresponding to residues 154-163 of human tissue factor (TF).

CC The peptide sequence contains a putative Factor X binding site.

CC The peptide is an inhibitor of TF-dependent coagulation in humans,
CC specifically the binding of TF-factor VIIa to factor X. It is useful
CC for treating or preventing blood clotting disorders or associated
CC problems in humans.

XX
SQ Sequence 10 AA;

Query Match 50.0%; Score 28; DB 18; Length 10;
Best Local Similarity 80.0%; Pred. No. 52;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YVWXS 14
DB 3 YVWXS 7

RESULT 13

AAW06151
ID AAW06151 standard; Peptide; 11 AA.

XX
AC AAW06151;

DT 16-AUG-1999 (first entry)

DE scFv 9A4 clone 15A VH CDR3 region.

XX Type II collagen; assay; antibody; rheumatoid arthritis;

XX osteoarthritis; diagnosis; monoclonal antibody; Mb; scFv;
XX single chain antibody; complementarity determining region; CDR;
XX mutant.

OS Mus musculus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "Ser in native sequence"

XX EP921395-A2.
 XX 09-JUN-1999.
 PD
 XX 12-NOV-1998; 98EP-0309266.
 PF
 XX 13-NOV-1997; 97US-0065423.
 PR
 XX (PFIZ) PFIZER PROD INC.
 PA
 XX Downs JT, Johnson KS, Mezes PS, Oterness IG;
 PI
 XX WPI, 1999-315488/27.
 DR
 XX
 XX Monitoring biological media for collagen fragments, using capture
 PT and/or detection antibodies
 CC
 XX Example 8; Page 30; 64pp; English.
 PS
 XX This sequence represents the mutated complementarity determining
 CC region CDR3 of the heavy chain variable region (VH) of single chain
 CC antibody scFv 9A4 clone 15A. It has a single amino acid difference
 CC from the parent clone (see AAY06150). A library of 9A4 scFvs was
 CC expressed in E. coli that carried mutated CDR3 sequences (see
 CC AAY06151-81). Binding studies to a collagen fragment demonstrated
 CC that changes could be made to the amino acid sequence of the parent
 CC scFv (see also AAY06130) while still retaining binding to the target.
 CC By altering different regions of 9A4 VH and VL, antibodies with
 CC variable to enhanced binding properties relative to the parent
 CC antibody can be produced. The invention provides a method for
 CC monitoring biological media for collagen II fragments, using capture
 CC and detection antibodies such as 9A4 and its engineered variants.
 CC The method can be used to assess the breakdown of type II collagen
 CC by collagenase in normal and pathological (rheumatoid arthritis,
 CC osteoarthritis) conditions.
 CC
 SQ Sequence 11 AA;
 Query Match 50.0%; Score 28; DB 20; Length 11;
 Best Local Similarity 80.0%; Pred. No. 57;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 LXYWM 12
 | | | |
 Db 7 LDYWM 11
 RESULT 14
 AAR55180
 ID AAR55180 standard; Protein; 13 AA.
 XX
 AC AAR55180;
 XX
 DT 19-JAN-1995 (first entry)
 XX
 DE huf binding site peptide analogue #2.
 XX
 KM Human; tissue factor; TF; heavy chain; pre-protein; pre-huTF; breast;
 KM soluble; huTF; hydrophobic; transmembrane; anchor region; monoclonal;
 KM aggregation; factor VII; factor VIIa; coagulation; antibody; MAb; assay;
 KM thrombus; detection; cancer; lung; carcinoma; anticoagulant; heparin.
 XX
 OS Synthetic.
 XX
 PM WO9411029-A.
 XX
 PD 26-MAY-1994.
 XX
 PF 16-NOV-1993; 93WO-US11239.
 XX
 PR 16-NOV-1992; 92US-0977281.
 XX

PA (SCRI) SCRIPPS RES INST.
 PA (UYDE-) UNIV PENNSYLVANIA.
 PA (UTEM) UNIV TEMPLE.
 XX
 PI Bernabei A, Colman RW, Edgington TS, Edmunds LH;
 PI Kapel Mayer J;
 DR WPI, 1994-183165/22.
 XX
 PT Inhibiting coagulation during extracorporeal circulation - by
 PT admin of monoclonal antibody preventing binding of tissue factor
 PT to coagulation factor 7 or 7a
 CC
 XX Disclosure; Page 5; 152pp; English.
 PS
 XX The sequences given in AAR55179-80 represent peptide analogues of the
 CC human tissue factor (huf) binding site. These peptides may be used to
 CC competitively inhibit the binding of huf to blood coagulation factor
 CC VII/VIIa, pref. without forming an activated complex, ie. without
 CC initiating coagulation.
 CC
 SQ Sequence 13 AA;
 Query Match 50.0%; Score 28; DB 15; Length 13;
 Best Local Similarity 80.0%; Pred. No. 68;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 YWXS 14
 | | | |
 Db 2 YWXS 6
 RESULT 15
 AAM98953
 ID AAM98953 standard; peptide; 13 AA.
 XX
 AC AAM98953;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Human tissue factor binding site peptide analogue #3.
 XX
 KM Human; tissue factor; huf; reperfusion damage; binding site;
 KM Factor VII; Factor VIIa; coagulation; anticoagulant; vasotropic;
 KM stroke; myocardial infarction; cerebral ischaemia.
 XX
 OS Homo sapiens.
 XX
 PM US5879677-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 13-JAN-1995; 95US-0372887.
 XX
 PR 09-DEC-1992; 92US-0987637.
 PR 13-JAN-1995; 95US-0372887.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Del Zoppo GJ;
 PI
 DR WPI, 1999-203904/17.
 XX
 PT Inhibiting tissue factor mediated reperfusion tissue damage
 PT following cerebral ischaemia or myocardial infarction - by the
 PT administration of tissue factor specific monoclonal antibodies to
 PT inhibit binding of the tissue factor to the Factor VII/VIIa complex
 XX
 PS Disclosure; Column 8; 29pp; English.
 XX
 CC A method has been developed for inhibiting tissue factor (TF) mediated
 CC cerebral reperfusion tissue damage in a subject with cerebral ischaemia
 CC (or one in which blood flow to the cerebral vessels has been occluded

CC during a surgical procedure) by the administration of monoclonal
CC antibodies similar to those produced by the cell lines ATCC HB9381,
CC HB9382 and/or HB9383 to inhibit blood coagulation reactions initiated by
CC the binding of TF to a Factor VII/VIIIa complex. The method can be used
CC to prevent damage caused by the reperfusion of blood into tissues
CC following, for example, a stroke, myocardial infarction or a surgical
CC procedure that resulted in the occlusion of blood flow to the tissue.
CC Reperfusion damage may be a result of TF mediated fibrin formation (i.e.
CC the beginning of the clot formation reaction), which contributes to the
CC no-reflow phenomenon by producing smaller secondary clots in capillaries
CC downstream from the original obstruction in response to vascular damage.
CC Treatment with the antibody prevents these clots from forming. AA98951
CC to AA98968 represent human TF binding site peptide analogues.

XX
SQ Sequence 13 AA;

Query Match 50.0%; Score 28; DB 20; Length 13;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14
| | | |
| | | |
DB 2 YWXS 6

Search completed: May 5, 2003, 14:11:50
Job time : 35 secs

GenCore version 5.1.4 p5 4578
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OM protein ~ protein search, using sw model

Run on: May 5, 2003, 14:13:46 ; Search time 44 Seconds
(without alignments)
27.455 Million cell updates/sec

Title: US-09-742-148a-3
Perfect score: 56
Sequence: 1 RXXLRIXLXYWXS 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 49618

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications AA.*
2: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_PEP.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	50.0	13	10	US-09-103-067-3
2	25	44.6	4	9	US-09-750-754-14
3	25	44.6	5	9	US-09-750-754-13
4	25	44.6	5	9	US-09-750-754-15
5	25	44.6	6	9	US-09-750-754-27
6	25	44.6	6	9	US-09-750-754-29
7	25	44.6	7	9	US-09-750-754-30
8	25	44.6	7	9	US-09-750-754-26
9	25	44.6	7	9	US-09-750-754-70
10	25	44.6	7	9	US-09-750-754-79
11	25	44.6	8	10	US-09-974-449-52
12	25	44.6	9	9	US-09-799-250-36
13	25	44.6	9	9	US-09-799-250-134
14	25	44.6	9	9	US-09-799-250-145
15	25	44.6	9	9	US-09-799-250-151
16	25	44.6	9	9	US-09-799-250-219
17	25	44.6	9	9	US-09-799-250-239
18	25	44.6	9	9	US-09-799-250-254
19	25	44.6	9	9	US-09-799-250-319

20	25	44.6	9	9	US-09-799-250-338	Sequence 338, App
21	25	44.6	9	9	US-09-799-250-344	Sequence 344, App
22	25	44.6	9	9	US-09-799-250-358	Sequence 358, App
23	25	44.6	9	9	US-09-799-250-423	Sequence 423, App
24	25	44.6	9	9	US-09-799-250-433	Sequence 433, App
25	25	44.6	9	9	US-09-799-250-442	Sequence 442, App
26	25	44.6	9	9	US-09-799-250-458	Sequence 458, App
27	25	44.6	9	9	US-09-799-250-555	Sequence 555, App
28	25	44.6	9	9	US-09-799-250-633	Sequence 633, App
29	25	44.6	9	9	US-09-799-250-636	Sequence 636, App
30	25	44.6	9	10	US-09-782-745-22	Sequence 22, App1
31	25	44.6	10	9	US-09-799-250-96	Sequence 96, App1
32	25	44.6	10	9	US-09-799-250-99	Sequence 99, App1
33	25	44.6	10	9	US-09-799-250-106	Sequence 106, App
34	25	44.6	10	9	US-09-799-250-169	Sequence 169, App
35	25	44.6	10	9	US-09-799-250-194	Sequence 194, App
36	25	44.6	10	9	US-09-799-250-280	Sequence 280, App
37	25	44.6	10	9	US-09-799-250-301	Sequence 301, App
38	25	44.6	10	9	US-09-799-250-381	Sequence 381, App
39	25	44.6	10	9	US-09-799-250-393	Sequence 393, App
40	25	44.6	10	9	US-09-799-250-405	Sequence 405, App
41	25	44.6	10	9	US-09-799-250-465	Sequence 465, App
42	25	44.6	10	9	US-09-799-250-474	Sequence 474, App
43	25	44.6	10	9	US-09-799-250-481	Sequence 481, App
44	25	44.6	10	9	US-09-799-250-508	Sequence 508, App
45	25	44.6	10	9	US-09-799-250-582	Sequence 582, App

ALIGNMENTS

RESULT 1
US-09-103-067-3
; Sequence 3, Application US/09103067
; Patent No. US20010048924A1
; GENERAL INFORMATION:
; APPLICANT: del Zoppo, Gregory J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF REPERFUSION DAMAGE
; FILE REFERENCE: scf2018s
; CURRENT APPLICATION NUMBER: US/09/103,067
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 08/372,887
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 07/987,637
; EARLIER FILING DATE: 1992-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human tissue
; OTHER INFORMATION: factor binding site polypeptide analog
US-09-103-067-3
Query Match 50.0%; Score 28; DB 10; Length 13;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 YWXS 14
DB 2 YWXS 6
RESULT 2
US-09-750-754-14
; Sequence 14, Application US/09750754
; Publication No. US20030055213A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu
; APPLICANT: MAKINO, Mika

APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Ieao
APPLICANT: TSUKUDA, Eiiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-14

Query Match 44.6%; Score 25; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 2 YW 4

RESULT 3
US-09-750-754-3
Sequence 3, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Ieao
APPLICANT: TSUKUDA, Eiiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-3

Query Match 44.6%; Score 25; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 3 YW 5

RESULT 4
US-09-750-754-15
Sequence 15, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Ieao
APPLICANT: TSUKUDA, Eiiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-15

Query Match 44.6%; Score 25; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 YYW 12
Db 3 YYW 5

RESULT 5
US-09-750-754-27
Sequence 27, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSES: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-27

Query Match 44.6%; Score 25; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 YYW 12
Db 4 YYW 6

RESULT 6
US-09-750-754-29
Sequence 29, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSES: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-29

Query Match 44.6%; Score 25; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 4 YW 6

RESULT 7
US-09-750-754-30
Sequence 30, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1h Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

US-09-750-754-30

Query Match 44.6%; Score 25; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 4 YW 6

RESULT 8
US-09-750-754-26
Sequence 26, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1h Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

US-09-750-754-26

Query Match 44.6%; Score 25; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 5 YW 7

RESULT 9
US-09-750-754-70
; Sequence 70, Application US/09750754
; Publication No. US20030055213A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu
; APPLICANT: MAKINO, Mika
; APPLICANT: CHIBA, Shigeru
; APPLICANT: KAWAMOTO, Isao
; APPLICANT: TSUKUDA, Eiji
; APPLICANT: YOSHIDA, Mayumi
; APPLICANT: BANDO, Chieko
; APPLICANT: YAMAGUCHI, Kazuo
; APPLICANT: MATSUDA, Yuzuru
; TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/750,754
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,625
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: TERRY, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 506.32366PX1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 7 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-09-750-754-70

Query Match 44.6%; Score 25; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 5 YW 7

RESULT 10
US-09-750-754-79
; Sequence 79, Application US/09750754
; Publication No. US20030055213A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu

APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-750-754-79

Query Match 44.6%; Score 25; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YW 12
DB 5 YW 7

RESULT 11
US-09-974-449-52
; Sequence 52, Application US/09974449
; Patent No. US20020141989A1
; GENERAL INFORMATION:
; APPLICANT: Krick, Franz
; APPLICANT: Stadler, Bodo
; APPLICANT: Vogel, Montague
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
; TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
; FILE REFERENCE: 4-30888A
; CURRENT APPLICATION NUMBER: US/09/974,449
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: PCT/EP00/03288
; PRIOR FILING DATE: 2000-04-12

```
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-449-52
```

```
Query Match      44.6%; Score 25; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 YYW 12
        |||
        5 YYW 7
```

```
RESULT 12
US-09-799-250-36
Sequence 36, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01
CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-36
```

```
Query Match      44.6%; Score 25; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 YYW 12
        |||
        5 YYW 7
```

```
RESULT 13
US-09-799-250-134
Sequence 134, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01
CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 134
LENGTH: 9
TYPE: PRT
```

```
ORGANISM: Homo sapiens
US-09-799-250-134
```

```
Query Match      44.6%; Score 25; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 YYW 12
        |||
        6 YYW 8
```

```
RESULT 14
US-09-799-250-145
Sequence 145, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01
CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-145
```

```
Query Match      44.6%; Score 25; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 YYW 12
        |||
        1 YYW 3
```

```
RESULT 15
US-09-799-250-151
Sequence 151, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01
CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-151
```

```
Query Match      44.6%; Score 25; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
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Mon May 5 13:59:05 2003

us-09-742-148a-3.closed.rapb

Page 7

Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	10	YTW	12						
Db	7	YTW	9						

Search completed: May 5, 2003, 14:18:38
Job time : 45 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 14:11:16 ; Search time 14 Seconds
(without alignments)
29.423 Million cell updates/sec

Title: US-09-742-148A-3
Perfect score: 56
Sequence: 1 RXXLRXLXYYWXS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 103252

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6ackfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	46	82.1	14	1	US-08-440-504A-3
2	46	82.1	14	4	US-08-433-613-3
3	41	73.2	10	4	US-08-433-613-57
4	41	73.2	14	4	US-08-433-613-17
5	41	73.2	14	4	US-08-433-613-18
6	35	62.5	13	4	US-08-433-613-19
7	31	55.4	13	4	US-08-433-613-20
8	31	55.4	13	4	US-08-433-613-21
9	30	53.6	14	4	US-08-433-613-16
10	28	50.0	10	2	US-08-479-223-1
11	28	50.0	13	2	US-08-372-887-3
12	27	48.2	14	4	US-08-433-613-10
13	27	48.2	14	4	US-08-433-613-35
14	27	48.2	14	4	US-08-433-613-36
15	27	48.2	14	4	US-08-433-613-41
16	26	46.4	10	1	US-08-222-851-13
17	26	46.4	10	1	US-08-222-851-30
18	26	46.4	10	1	US-08-440-504A-4
19	26	46.4	10	1	US-08-440-504A-5
20	26	46.4	10	4	US-08-651-650-12
21	26	46.4	10	4	US-08-651-650-15
22	26	46.4	10	5	PCT-US94-12985-9
23	26	46.4	10	5	PCT-US94-12985-12
24	26	46.4	14	4	US-08-433-613-4
25	26	46.4	14	4	US-08-433-613-7
26	26	46.4	14	4	US-08-433-613-14
27	26	46.4	14	4	US-08-433-613-55

28	25	44.6	3	1	US-08-440-504A-1	Sequence 1, Appl
29	25	44.6	3	4	US-08-433-613-1	Sequence 1, Appl
30	25	44.6	4	1	US-08-321-625-14	Sequence 14, Appl
31	25	44.6	4	1	US-08-440-504A-2	Sequence 2, Appl
32	25	44.6	4	4	US-08-433-613-2	Sequence 14, Appl
33	25	44.6	5	1	US-08-321-625-3	Sequence 3, Appl
34	25	44.6	5	1	US-08-321-625-15	Sequence 15, Appl
35	25	44.6	5	4	US-09-181-083-3	Sequence 3, Appl
36	25	44.6	5	4	US-09-181-083-15	Sequence 15, Appl
37	25	44.6	5	4	US-08-918-148-43	Sequence 43, Appl
38	25	44.6	6	1	US-08-321-625-27	Sequence 27, Appl
39	25	44.6	6	1	US-08-321-625-29	Sequence 30, Appl
40	25	44.6	6	1	US-08-321-625-30	Sequence 295, App
41	25	44.6	6	2	US-08-637-7598-295	Sequence 295, App
42	25	44.6	6	3	US-08-871-355A-295	Sequence 27, Appl
43	25	44.6	6	4	US-09-181-083-27	Sequence 29, Appl
44	25	44.6	6	4	US-09-181-083-29	
45	25	44.6	6	4	US-09-181-083-29	

ALIGNMENTS

RESULT 1
US-08-440-504A-3
Sequence 3, Application US/08440504A
Patent No. 5753625
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Treatment for Inhibiting the Progression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Flehr, Holbach, Teest, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,504A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /note="The 'X' at position can
OTHER INFORMATION: either be Valine or Glutamic Acid."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="The 'X' at position three
OTHER INFORMATION: can either be Asparagine or Aspartic Acid."

NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "The 'X' at position 7 can
OTHER INFORMATION: either be Alanine or Leucine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "The 'X' at position 9 can
OTHER INFORMATION: either be Arginine or Glutamic Acid."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note= "The 'X' at position 13 can
OTHER INFORMATION: either be Glutamine or Aspartic Acid."
US-08-440-504A-3

Query Match 82.1%; Score 46; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXXLRILXLYWXS 14
DB 1 RXXLRILXLYWXS 14

RESULT 2
US-08-433-613-3
Sequence 3, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RFT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (2)
OTHER INFORMATION: The amino acid at position 2 can be either Valine
OTHER INFORMATION: or Glutamic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (3)
OTHER INFORMATION: The amino acid at position 3 can be either
OTHER INFORMATION: Asparagine or Aspartic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
OTHER INFORMATION: The amino acid at position 7 can be either Alanine
OTHER INFORMATION: or Leucine.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (9)
OTHER INFORMATION: The amino acid at position 9 can be either
OTHER INFORMATION: Arginine or Glutamic acid.
FEATURE:
NAME/KEY: UNSURE
LOCATION: (13)
OTHER INFORMATION: The amino acid at position 13 can be either
OTHER INFORMATION: Glutamine or Aspartic acid.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-3

Query Match 82.1%; Score 46; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXXLRILXLYWXS 14
DB 1 RXXLRILXLYWXS 14

RESULT 3
US-08-433-613-57
Sequence 57, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RFT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-57

Query Match 73.2%; Score 41; DB 4; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.085;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIIXLYW 12
DB 2 LRIALRYW 10

RESULT 4
US-08-433-613-17
Sequence 17, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
FILE REFERENCE: A61008/RFT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-17

Query Match 73.2%; Score 41; DB 4; Length 14;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRIIXLYW 12
DB 6 LRIALRYW 14

RESULT 5
US-08-433-613-18
Sequence 18, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland


```

; TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
; FILE OF INVENTION: Activity
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-18

Query Match      73.2%; Score 41; DB 4; Length 14;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRLXLYYW 12
Db 5 LRLXLYYW 13

RESULT 6
US-08-433-613-19
; Sequence 19, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-19

Query Match      62.5%; Score 35; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 IXLXYYWXS 14
Db 5 IALRYWDS 13

RESULT 7
US-08-433-613-20
; Sequence 20, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

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US-08-433-613-20

Query Match      55.4%; Score 31; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 LXYWXS 14
Db 6 LRYWDS 12

RESULT 8
US-08-433-613-21
; Sequence 21, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-21

Query Match      55.4%; Score 31; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 LXYWXS 14
Db 5 LRYWDS 11

RESULT 9
US-08-433-613-16
; Sequence 16, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cycomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-16

Query Match      53.6%; Score 30; DB 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRLXLYYW 11
Db 7 LRLXLYYW 14

RESULT 10
US-08-479-223-1

```

Sequence 1, Application US/08479223
Patent No. 5837684
GENERAL INFORMATION:
APPLICANT: ORNING, Lars
APPLICANT: ARBO, Bente
APPLICANT: FISCHER, Peter
APPLICANT: SAKARIASSEN, Kjell S.
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slater Lane - 4th Floor
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,223
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/Orning
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-683-0500
TELEFAX: 703-683-1080
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-479-223-1

Query Match 50.0%; Score 28; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14
Db 3 YWXS 7

RESULT 11
US-08-372-887-3
Sequence 3, Application US/08372887
Patent No. 5879677
GENERAL INFORMATION:
APPLICANT: del Zoppo, Gregory J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF REPERFUSION
TITLE OF INVENTION: DAMAGE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,887
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,637
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..13
US-08-372-887-3

Query Match 50.0%; Score 28; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 YWXS 14
Db 2 YWXS 6

RESULT 12
US-08-433-613-10
Sequence 10, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cyomodulating Peptide for Inhibiting Lymphocyte
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: A61008/RT/TAL
CURRENT APPLICATION NUMBER: US/08/433,613A
CURRENT FILING DATE: 1995-05-03
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-10

Query Match 48.2%; Score 27; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RXLRILXY 10
Db 5 RSLRLRLRY 14

RESULT 13
US-08-433-613-35
Sequence 35, Application US/08433613A
Patent No. 6162434
GENERAL INFORMATION:
APPLICANT: Buelow, Roland
TITLE OF INVENTION: Cyomodulating Peptide for Inhibiting Lymphocyte

```

; TITLE OF INVENTION: Activity
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-35

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Query Match
Best Local Similarity 48.2%; Score 27; DB 4; Length 14;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 RXXLRIXLXY 10
| | | | |
DB 5 RANLRIRALRY 14

```

```

RESULT 14
US-08-433-613-36
; Sequence 36, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-36

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```

Query Match
Best Local Similarity 48.2%; Score 27; DB 4; Length 14;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 RXXLRIXLXY 10
| | | | |
DB 5 RANLRIRALRY 14

```

```

RESULT 15
US-08-433-613-41
; Sequence 41, Application US/08433613A
; Patent No. 6162434
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; TITLE OF INVENTION: Cytomodulating Peptide for Inhibiting Lymphocyte
; FILE REFERENCE: A61008/RFT/TAL
; CURRENT APPLICATION NUMBER: US/08/433,613A
; CURRENT FILING DATE: 1995-05-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-433-613-41

```

```

Query Match
Best Local Similarity 48.2%; Score 27; DB 4; Length 14;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 RXXLRIXLXY 10
| | | | |
DB 5 RANLRIRALRY 14

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Search completed: May 5, 2003, 14:14:48
Job time : 15 secs

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